

GenCore version 5.1.9  
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nucleic - nucleic search, using sw model

on: June 4, 2006, 21:35:04 ; Search time 5078 Seconds  
(without alignments)  
6938.761 Million cell updates/sec

US-10-089-641-1

net score: 551

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ing table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

ched: 6366136 seqs, 31973710525 residues

1 number of hits satisfying chosen parameters: 12732272

num DB seq length: 0

num DB seq length: 200000000

rocessing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

base :

GenEmbl:\*  
1: gb env:\*  
2: gb pac:\*  
3: gb ph:\*  
4: gb pl:\*  
5: gb pr:\*  
6: gb ro:\*  
7: gb sts:\*  
8: gb sy:\*  
9: gb un:\*  
10: gb vi:\*  
11: gb ov:\*  
12: gb htg:\*  
13: gb ln:\*  
14: gb om:\*  
15: gb ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score	Query Match	Length	ID	Description
551	100.0	551	AF078078	Homo sapi
542	98.4	1065	AR035810	Sequence
542	98.4	1065	AR035837	Sequence
542	98.4	1065	AR342089	Sequence
542	98.4	1066	AF079806	Homo sapi
542	98.4	1066	BC019325	Homo sapi
542	98.4	1077	BC000465	Homo sapi
542	98.4	1078	CQ776351	Sequence
542	98.4	1078	CS020434	Sequence
542	97.8	1036	E13578	Human mRNA
538.8	97.8	1036	D83023	Homo sapien
538.8	97.8	1036	CQ724300	Sequence
531	96.4	1066	AF087883	Homo sapi
530.6	96.3	1060	AR380275	Sequence
527.8	95.8	750	BT007234	Homo sapi
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22	477	86.6	477	2	AR035854	Sequence
23	476.8	86.5	480	5	CR457038	Homo sapi
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25	473.8	86.0	477	2	E13577	Human mRNA
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#### ALIGNMENTS

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DEFINITION	Homo sapiens growth arrest and DNA-damage-inducible protein				
ACCESSION	GADD45gamma mRNA, complete cds.				
VERSION	AF078078.1	GI:3978393			
KEYWORDS					
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 551)				
AUTHORS	Takekawa, M. and Saito, H.				
TITLE	A family of stress-inducible GADD45-like proteins mediate				
JOURNAL	Cell 95 (4), 521-530 (1998)				
PUBMED	9827804				
REFERENCE	2 (bases 1 to 551)				
AUTHORS	Takekawa, M. and Saito, H.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-JUL-1998) Dana-Farber Cancer Institute, Harvard				
Medical School, 44 Binney Street, Boston, MA 02115, USA					
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BC019325 1068 bp mRNA linear PRI 29-JUN-2004  
Homo sapiens growth arrest and DNA-damage-inducible, gamma, mRNA  
(CDNA clone MGC:4374 IMAGE:2823131), complete cds.  
BC019325  
BC019325.1 GI:17939520  
MGC.  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 1068)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schlier, G.D.,  
Hopkins, R.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

REMARK  
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaabs-remail.nih.gov](mailto:cgaabs-remail.nih.gov)  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth  
Featherstone, Malachi Griffith, Odi Griffith, Ran Guin, Nancy Liao,  
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Worth,  
Telka Olson, Diana Palmquist, Anca Petrescu, Anna Lilia Prabhu,  
Paraneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,  
Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacque  
Schein, Asim Siddiqui, Rob Holt, Marco Marr.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LINL at: <http://image.linl.gov>  
Series: IRAL Plate: 9 Row: c Column: 10  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 9790905.

FEATURES

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CDS

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: CQ776351 1078 bp DNA linear PAT 11-MAR-2004
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: Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
: Homiidae; Homo.
: ENCE
: HORS 1
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LOCUS CS020434
DEFINITION Sequence 9 from Patent EP1506784.
ACCESSION CS020434
VERSION CS020434.1 GI:60221058
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homiidae; Homo.
REFERENCE
1 Franzoso, G., Desmarteis, E., Zazzeroni, F., Papa, S. and Bubbici, C.
AUTHORS Identification of novel factors that block programmed cell death or
TITLE apoptosis by targeting JNK
JOURNAL Patent: EP 1506784-A 9 16-FEB-2005;
UNIVERSITY University of Chicago (US)
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Best Local Similarity 100.0%; Pred. No. 6.3e-125;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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78
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Homidae; Homo.
1 (bases 1 to 1036)
RENCE Suzuki,M., Watanabe,T. and Fujiwara,T.
THORS GRP17 GENE
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URNAL OTSUKA PHARMACEUT CO LTD
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PN JP 1997206083-A/2
PD 12-AUG-1997
PF 09-FEB-1996 JP 1996023612
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DEFINITION DB3023.1 GI:5913968
ACCESSION DB3023.1
VERSION GRP17; gadd45-related protein.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1036)
REFERENCE Suzuki,M., Watanabe,T.K., Fujiwara,T., Nakamura,Y.P.6., Takahashi,E.
AUTHORS and Tanigami,A.
TITLE Molecular cloning, expression, and mapping of a novel human cDNA,
JOURNAL GRP17, highly homologous to human gadd45 and murine MyD118
PUBMED 10496071
REFERENCE 2 (bases 1 to 1036)
AUTHORS Watanabe,T.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-1996) Takeshi Watanabe, Otsuka Pharmaceutical

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Co., Ltd. Otsuka GEN Research Institute; 463-10 Kagasuno  
Kawachi-cho, Tokushima, Tokushima 771-01, Japan (Tel:0886-65-2888,  
Fax:0886-37-1035)

Location/Qualifiers  
source 1.1036

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CDS

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ATVAGEEAGAPEDLHCLITSNPNEADAMKDPALKEKSLFCESRSVNDVPSITLPE"

Query Match 97.8%; Score 538.8; DB 5; Length 1036;  
Best Local Similarity 99.6%; Pred. No. 4e-124;  
Matches 540; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CTGGTTGATGCACTATGACTGTGAAAGATCCGGGCGGAGACACAGTTCCGGAAGC 60  
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61 ACAGCCAGGATGAGGGGTCGGGAAAGGCTGATGATGTTGCTGTCGGGCGAGCGT 120  
129 ACAGCCAGGATGAGGGGTCGGGAAAGGCTGATGATGTTGCTGTCGGGCGAGCGT 188  
121 CAGGGCTGCTCACTGCGCGGCTCTACAGTCAAGCCAAAGTCTTGAACGTGACCCGAC 180  
189 CAGGGCTGCTCACTGCGCGGCTCTACAGTCAAGCCAAAGTCTTGAACGTGACCCGAC 248  
181 AATGTACCTTCTGTGTGCTGCTGCGGCTGAGAGAGACAGGGCGACATCCGCTGCA 240  
249 AATGTACCTTCTGTGTGCTGCTGCGGCTGAGAGAGACAGGGCGACATCCGCTGCA 308  
241 ATCCATTTTAAAGCTGATCCAGGCTTCTGCTGAGAGACAGATGACATATAGTGGCG 300  
309 ATCCATTTTAAAGCTGATCCAGGCTTCTGCTGAGAGACAGATGACATATAGTGGCG 368  
301 GGGGATGTGACGCGCTGCGGCTATCTGAGCGCCGCGAGAGCGGGTGCAGCCGAC 360  
369 GGGGATGTGACGCGCTGCGGCTATCTGAGCGCCGCGAGAGCGGGTGCAGCCGAC 428  
361 GACCTGCATGCACTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 420  
429 GACCTGCATGCACTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 488  
421 GAGAACTCAGCCTGTTTTCGAGAGAGAGCGGAGGCTTAAAGCACTGGGAGCCAGATC 480  
489 GAGAACTCAGCCTGTTTTCGAGAGAGAGCGGAGGCTTAAAGCACTGGGAGCCAGATC 548  
481 ACCCTCCCGAGTGAACGCCGCGGAGACCTTGTCTGATCGACGTGTGACGCCCGG 540  
549 ACCCTCCCGAGTGAACGCCGCGGAGACCTTGTGTGATCGACGTGTGACGCCCGG 608  
541 GG 542  
609 GG 610

1066 bp DNA linear PAT 03-FEB-2004  
Sequence 10234 from Patent WO02068579.  
CQ724300  
CQ724300  
CQ724300.1 GI:42285157

KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

REFERENCE  
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.  
TITLE Kites, such as nucleic acid arrays, comprising a majority of  
humanecons or transcripts, for detecting expression and other uses  
thereof

JOURNAL Patent: WO 02068579-A 10234 06-SEP-2002;

FEATURES  
source PE Corporation (NY) (US)  
Location/Qualifiers  
1.1066  
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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 3.6e-122;  
Matches 542; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 CTGGTTGATGCACTATGACTGTGAAAGATCCGGGCGGAGACACAGTTCCGGAAGC 60  
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61 ACAGCCAGGATGAGGGGTCGGGAAAGGCTGATGATGTTGCTGTCGGGCGAGCGT 120  
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121 CAGGGCTGCTCACTGCGCGGCTCTACAGTCAAGCCAAAGTCTTGAACGTGACCCGAC 179  
215 CAGGGCTGCTCACTGCGCGGCTCTACAGTCAAGCCAAAGTCTTGAACGTGACCCGAC 274  
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275 CAATGTACCTTCTGTGTGCTGCTGCGGCTGAGAGAGACAGGGCGACATCCGCTGCA 334  
240 GATTCATTTTAAAGCTGATCCAGGCTTCTGCTGAGAGACAGATGACATATAGTGGCG 299  
335 GATTCATTTTAAAGCTGATCCAGGCTTCTGCTGAGAGACAGATGACATATAGTGGCG 394  
300 GGGGATGTGACGCGCTGCGGCTATCTGAGCGCCGCGAGAGCGGGTGCAGCCGAC 359  
395 GGGGATGTGACGCGCTGCGGCTATCTGAGCGCCGCGAGAGCGGGTGCAGCCGAC 454  
360 CGACCTGCATGCACTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTT 419  
455 CGACCTGCATGCACTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTT 514  
420 GAGAACTCAGCCTGTTTTCGAGAGAGAGCGGAGGCTTAAAGCACTGGGAGCCAGAT 479  
515 GAGAACTCAGCCTGTTTTCGAGAGAGAGCGGAGGCTTAAAGCACTGGGAGCCAGAT 574  
480 CACCTCCCGAGTGAACGCCGCGGAGACCTTGTCTGATCGACGTGTGACGCCCGG 539  
575 CACCTCCCGAGTGAACGCCGCGGAGACCTTGTGTGATCGACGTGTGACGCCCGG 634  
540 GG 542  
635 GG 637

RESULT 13  
AF087883 1066 bp mRNA linear PRI 01-FEB-2001  
LOCUS AF087883  
DEFINITION Homo sapiens growth arrest and DNA damage inducible protein gamma  
(GADD45G) mRNA, complete cds.  
ACCESSION AF087883  
VERSION AF087883.1 GI:12642943  
KEYWORDS



	CE	Homo sapiens (human)
JANISM	Homo sapiens	
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
	Hominidae; Homo.	
RENCE	1 (bases 1 to 1060)	
THORS	Gong, R., Yu, L., Zhang, H., Tu, Q., Zhao, Y., Yang, J., Xu, Y. and	
	Zhao, S.	
TLE	Assignment of human GADD45G to chromosome 9q22.1-->q22.3 by	
	radiation hybrid mapping	
URNAL	Cytogenet. Cell Genet. 88 (1-2), 95-96 (2000)	
(UNMED	107367	
RENCES	2 (bases 1 to 1060)	
THORS	Li, N.G., Yu, L., Zhou, Y., Zhang, H.L., Han, X.F. and Zhao, S.Y.	
TLE	Direct Submission	
URNAL	Submitted (37-AUG-1998) Lab of Human Gene Research, Institute of	
	Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,	
	P.R. China	
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CDS	96..575	
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st Local Similarity	98.3%; Pred. No. 4.5e-122;	
tches 536; Conservative	0; Mismatches 9; Indels 0; Gaps 0;	
1	CTGTGTTATGCCACTATGACTCTTGGAAGAAGTCGCGGCAGAGACACAGTTCGGGAAGC	60
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321	ATTCATTTTACGCTGATTCAGGCTTTCTGCTGCGAAGACGACATGACATAGTGGCGTG	380
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361	GACCTGCACTGATCTCATTTTGAACCCCAACGAGAGCGCTGGAAGATCCCGCTTG	420
441	GACCTGCACTGATCTCATTTTGAACCCCAACGAGAGCGCTGGAAGATCCCGCTTG	500
421	GGAAGCTCACGCTTTTTGCGAAGAGACGCGACGCTTAAAGACTGGGGTGCACAGATC	480
501	GGAAGCTCACGCTTTTTGCGAAGAGACGCGACGCTTAAAGACTGGGGTGCACAGATC	560

Qy	481	ACCTCTCCCGAGTGACAGCCCGCGGGAGCCTTGCTGTATCGAGCTGTGACGCCCCCGG	540
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LOCUS	AR380275	750 bp	DNA
DEFINITION	Sequence 820 from patent US 6607879.		
ACCESSION	AR380275		
VERSION	AR380275.1	GI:4087909	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 750)		
AUTHORS	Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.		
TITLE	Compositions for the detection of blood cell and immunological response gene expression		
JOURNAL	Patent: US 6607879-A 820 19-AUG-2003;		
FEATURES	Incyte Corporation; Palo Alto, CA		
source	1..750		
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	/mol_type="genomic DNA"		
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Best Local Similarity	99.4%;	Pred. No. 2.4e-121;	
Matches	540;	Conservative	0; Mismatches 2; Indels 1; Gaps 1
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Db	564	CACCTTCCCGAGTGACAGCCCGCGGGAGCCTTGGTCTGATCGACGTGTGACACGCCCGG	623
Qy	540	GGG	542

624 GGG 626

T 15  
234  
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Homo sapiens growth arrest and DNA-damage-inducible, gamma mRNA,  
complete cds.  
BT007234  
BT007234.1 GI:30583306  
FLI\_CDNA.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 480)  
Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
Pheasant,M. and Farmer,A.  
Cloning of human full-length cDNAs in BD Creator(TM) System Donor  
vector  
Unpublished  
2 (bases 1 to 480)  
Kalline,N., Chen,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S.,  
Koundinya,M., Raphael,J., Moreira,D., Kelley,T., Labaer,J., Lin,Y.,  
Pheasant,M. and Farmer,A.  
Direct Submission  
Submitted (13-MAY-2003) BD Biosciences Clontech, 1020 East Meadow  
Circle, Palo Alto, CA 94303, USA  
This CDS clone is a part of a collection of human full length  
expression clones generated by BD Biosciences Clontech and the  
Harvard Institute of Proteomics. Each CDS has been cloned in two  
forms: with and without stop-codon (to allow fusion with C-terminal  
tag). The CDS has been directionally cloned using BD In-Fusion(TM)  
cloning system between the SalI and HindIII sites of the pDNR-DUAL  
vector. Additional sequences in the clone: 'ACC' after SalI site  
and before 'ATG' to provide Kozak consensus sequence; 'GG' after  
last codon and before HindIII site to maintain reading frame.  
Clone distribution: <http://bioinfo.clontech.com/orfclones>.  
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CDS

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ry Match 86.8%; Score 478; DB 5; Length 480;  
Local Similarity 100.0%; Pred. No. 7.9e-109; Indels 0; Gaps 0;  
ches 478; Conservative 0; Mismatches 0;

16 ATGACTCTGGAAGAAGTCCGGCCGACAGACAGTTCGGAAAGCAAGCCAGAGATGACG 75  
1 ATGACTCTGGAAGAAGTCCGGCCGACAGACAGTTCGGAAAGCAAGCCAGAGATGACG 60  
76 GGTGCCGGGAAAGCGCTGATGAGTTGCTGCTGCGCGCAGCGTCAAGGCTGCTCACT 135  
61 GGTGCCGGGAAAGCGCTGATGAGTTGCTGCTGCGCGCAGCGTCAAGGCTGCTCACT 120

QY 136 GCGGCGCTTACAGATCAGCCAAAGCTTTGAACGTGAGACCCCGCAATATGACCTTCGT 195  
DB 121 GCGGCGCTTACAGATCAGCCAAAGCTTTGAACGTGAGACCCCGCAATATGACCTTCGT 180  
QY 196 GGTGCGGCTGCGGGGTGAGAGAGAGAGGCGACATCGCGCTGCAGATTCATTTTACGCTG 255  
DB 181 GTGCTGGCTGCGGGGTGAGAGAGAGAGGCGACATCGCGCTGCAGATTCATTTTACGCTG 240  
QY 256 ATCAAGGCTTTTGTGCTGCGAAGACATGACATAGTGGCGTGGCGATGTGACGCGG 315  
DB 241 ATCAAGGCTTTTGTGCTGCGAAGACATGACATAGTGGCGTGGCGATGTGACGCGG 300  
QY 316 CTGCGGCGCTATGTGGGCGCGCGCGAGAGAGGCGGCTGCGCGGCGACCTGACATGCAATC 375  
DB 301 CTGCGGCGCTATGTGGGCGCGCGCGAGAGAGGCGGCTGCGCGGCGACCTGACATGCAATC 360  
QY 376 CTCAATTTGAACCCCAAGAGAGAGCGCTTGAAGATCCCGCTTGAGAAAGCTCAGCCGTG 435  
DB 361 CTCAATTTGAACCCCAAGAGAGAGCGCTTGAAGATCCCGCTTGAGAAAGCTCAGCCGTG 420  
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DB 421 TTTTGGAGAGAGAGCGCGAGCGTTAAGCATGCGGTGCGCCAGCATCACTCCCGAGT 478

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GenCore version 5.1.9  
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nucleic - nucleic search, using sw model

on: June 4, 2006, 21:33:54 ; Search time 643 Seconds

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9: geneseqn2003bs:\*  
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15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

lc	Score	Query	Match	Length	ID	Description
1	542	98.4	1056	14	AED73447	Aed73447 Human pla
2	542	98.4	1065	2	AAT43381	Aat43381 Human cyt
3	542	98.4	1065	3	AAA39665	Aaa39665 Human CR6
4	542	98.4	1066	3	AAA64826	Aaa64826 Human SYG
5	542	98.4	1066	11	ADP65476	Adp65476 Human cyt
6	542	98.4	1078	8	ACC59049	Acc59049 Human Gad
7	542	98.4	1078	11	ADP65003	Adp65003 Human giro
8	542	98.4	1078	12	ADJ74785	Adj74785 Marker ge
9	542	98.4	1078	13	ADR25449	Adr25449 Breast ca
10	542	98.4	1078	14	ADX85165	Adx85165 Human gad
11	537.2	97.5	1036	2	AAT74048	Aat74048 Human GRP
12	527.8	95.8	750	11	ADJ31494	Adj31494 Human CDN
13	527.8	95.8	750	13	ADS83561	Ads83561 Human lym
14	525.4	95.4	612	12	ADQ20819	Adq20819 Human sof
15	512.8	93.1	1202	12	ADQ24782	Adq24782 Human sof
16	480	87.6	480	14	ADVA3063	Adv43063 Human psy
17	477	86.6	477	3	AAA39682	Aaa39682 Cytokine
18	477	86.6	1302	11	ACN44751	Acn44751 Human mRN

19	472.2	85.7	477	2	AAT74047	Aat74047 Human GRP
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21	431.4	78.3	1084	8	ACC59050	Acc59050 Mouse Gad
22	431.4	78.3	1084	12	ADJ75713	Adj75713 Marker ge
23	431.4	78.3	1084	14	ADX85167	Adx85167 Mouse gad
24	427	77.5	555	14	ADV77129	Adv77129 Huntingro
25	423.6	76.9	574	11	ACN44749	Acn44749 Mouse mRN
26	405.8	73.6	574	10	ADD34070	Add34070 Mouse mit
27	372	67.5	1284	3	AAC59606	Aac59606 Human sec
28	343.8	62.4	816	15	AEF75388	Aef75388 Human pol
29	295.8	53.7	503	6	ABF199870	Abf199870 Mouse isc
30	274	49.7	4444	6	ABF156856	Abf156856 Gadd45-ga
31	274	49.7	21543	11	ACN44750	Acn44750 Human gen
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34	180.4	32.7	480	14	AED73625	Aed73625 Human pla
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41	180.4	32.7	1374	2	AAZ42213	Aaz42213 Human nor
42	180.4	32.7	1374	13	ADP24253	Adp24253 PRO polyP
43	180.4	32.7	1378	14	ADY16172	Ady16172 DNA encod
44	180.4	32.7	518	14	ACU55905	Acu55905 Human col
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## ALIGNMENTS

RESULT 1  
ID AED73447/c  
AED73447 standard; cDNA; 1056 BP.  
AC AED73447:  
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XX 12-JUN-2006 (first entry)  
XX  
XX Human placental protein encoding cDNA SEQ ID NO:275.  
XX  
XX  
XX  
XX Homo sapiens.  
XX  
XX OS  
XX PN US2005255114-A1.  
XX PD 17-NOV-2005.  
XX  
XX 07-APR-2004; 2004US-00821234.  
XX PF 07-APR-2003; 2003US-0462047P.  
XX PR  
XX (NUVE-) NUVELO INC.  
XX  
XX Labat I, Tang YT, Seache-Crain B, Boyle B;  
XX WPI: 2005-808574/82.  
XX DR P-PSDB; AED74299.  
XX  
XX Identifying a patient with a higher risk of preeclampsia comprises  
XX nucleic acid hybridization assay or antibody assay to determine level of  
XX a specific nucleic acid (mRNA) or polypeptide.  
XX  
XX Claim 1; SEQ ID NO 275; 358pp; English.  
XX  
XX The invention relates to a method for identifying a patient with a higher  
XX risk of preeclampsia. The method comprises: (a) assaying a sample from  
XX the patient to determine the level of a mRNA or other polynucleotide of  
XX within the sample that hybridizes specifically to a polynucleotide of  
XX AED73373-AED74024, and comparing the level to a standard; or (b)  
XX contacting a sample from the patient with an antibody that specifically

binds to a polypeptide of AED74025-AED74876 to determine the level of polypeptide within the sample, and comparing the level to a standard. Also described: (1) a diagnostic kit, for detecting preclampsia, comprising: (a) an antibody specific for any of the polypeptides of AED74025-AED74876 or their fragments; or (b) a polynucleotide sequence comprising any of AED73173-AED74024 coupled to a surface; and (c) a standard for any of the polypeptides of AED74025-AED74876 or any of the polynucleotides of AED73173-AED74024 indicative of a higher risk of diagnosis of preclampsia; (2) a pharmaceutical composition comprising an antibody specific for any of the polypeptides of AED74025-AED74876 or one or more purified polypeptides of AED74025-AED74876, to ameliorate signs or symptoms of preclampsia; and (3) a method of treating preclampsia. The method and kit are useful for identifying a patient with a higher risk of preclampsia. The composition and method are useful for treating preclampsia. The present sequence represents a nucleic acid sequence obtained from a human placental cDNA library. Note - The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.

Sequence 1056 BP; 193 A; 376 C; 292 G; 195 T; 0 U; 0 Other;

Query Match 98.4%; Score 542; DB 14; Length 1056;

Local Similarity 100.0%; Pred. No. 5.8e-113; Indels 0; Gaps 0;

ches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGGTTGATCGCACTATGACTGTGAAAGATCCCGGCGGAGACACAGTTCCGAAAGC 60  
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980 CTGGTTGATCGCACTATGACTGTGAAAGATCCCGGCGGAGACACAGTTCCGAAAGC 921  
|||||  
61 ACAGCCAGATGAGGAGTCCGGGAAAGGCGTCATGATGTTGCTGTCGCGGACGCT 120  
|||||  
920 ACAGCCAGATGAGGAGTCCGGGAAAGGCGTCATGATGTTGCTGTCGCGGACGCT 861  
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121 CAGGGCTGCTCACTGCGCGGCTCTACAGAGTCAGCCAAAGTCTGAACGTCGACCCGAC 180  
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860 CAGGGCTGCTCACTGCGCGGCTCTACAGAGTCAGCCAAAGTCTGAACGTCGACCCGAC 801  
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181 AATGTGACCTTCTGTGTGCTGCTGCGGTGAGAGAGACAGGCGCATCGGCTGCAG 240  
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800 AATGTGACCTTCTGTGTGCTGCTGCGGTGAGAGAGACAGGCGCATCGGCTGCAG 741  
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241 ATCCATTTTACGCTGATCCAGGCTTCTGCTGCGAGAGACATCGCATAGTGCAGTG 300  
|||||  
740 ATCCATTTTACGCTGATCCAGGCTTCTGCTGCGAGAGACATCGCATAGTGCAGTG 601  
|||||  
301 GGGGATGTGACAGGCTGCGGCTATCTGTGGGCGCGGCGAGAGGCGGGTGCAGCG 360  
|||||  
680 GGGGATGTGACAGGCTGCGGCTATCTGTGGGCGCGGCGAGAGGCGGGTGCAGCG 621  
|||||  
361 GACCTGACATGCTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGGCTTG 420  
|||||  
620 GACCTGACATGCTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGGCTTG 501  
|||||  
421 GAGAGCTGACGCTGTTTTCGAGAGAGCGGAGCGCTTAACAGATGCGGTCACAGAT 480  
|||||  
560 GAGAGCTGACGCTGTTTTCGAGAGAGCGGAGCGCTTAACAGATGCGGTCACAGAT 501  
|||||  
481 ACCCTCCCGAGTGAAGAGCCCGGCGGAGCTTGTGTGATGACGTCGACGCGCCG 540  
|||||  
500 ACCCTCCCGAGTGAAGAGCCCGGCGGAGCTTGTGTGATGACGTCGACGCGCCG 441  
|||||  
541 GG 542  
|||||  
440 GG 439

1381  
J12  
AAT43381 standard, cDNA; 1065 BP.

AAT43381;

11-MAR-1997 (first entry)

XX DE Human cytokine response gene CR6.  
XX KW Cytokine response gene; CR6; interleukin-2; IL-2;  
XX KW ligand-stimulated gene expression; diagnosis; therapy; ss.  
XX OS Homo sapiens.  
XX PH Key  
XX FT CDS Location/Qualifiers  
XX FT 98..577  
XX FT /\*tag= a  
XX PN M09639427-A1.  
XX PD 12-DEC-1996.  
XX PF 05-JUN-1996; 96WO-US009194.  
XX PR 05-JUN-1995; 95US-00461379.  
XX PR 05-JUN-1995; 95US-00462337.  
XX PR 05-JUN-1995; 95US-00462390.  
XX PR 05-JUN-1995; 95US-00463074.  
XX PR 05-JUN-1995; 95US-00463081.  
XX PR 05-JUN-1995; 95US-00465585.  
XX PA (DART-) DARTMOUTH COLLEGE.  
XX PI Smith KA, Beadling C;  
XX DR WPI; 1997-043062/04.  
XX DR P-PSDB; AAW08138.  
XX PT Cytokine response proteins and genes - used in the detection and therapy  
XX PT of diseases caused by a mutation in the CR coding region.  
XX PS Disclosure; Page 29-20; 81bp; English.  
XX CC 8 clones (AAT43376-83) confg. interleukin-2 (IL-2)-induced genes were  
XX CC isolated from a human IL2 receptor-positive T blast cell cDNA library  
XX CC following IL-2 stimulation. 6 Of these ligand-induced genes (CR1, 2, 3,  
XX CC 5, 6, 8) are novel. The CR6 gene encodes a 17.5 kDa protein (AAW08138)  
XX CC that may facilitate cellular proliferation by preventing the inhibitory  
XX CC activity of p21. Expression is suppressed by elevated cAMP. CR genes and  
XX CC polypeptides (AAW08133-40) are useful as diagnostic or therapeutic agents  
XX CC ; CR gene sequences can be used to detect and treat allelic mutations  
XX SQ Sequence 1065 BP; 198 A; 293 C; 378 G; 196 T; 0 U; 0 Other;

Query Match 98.4%; Score 542; DB 2; Length 1065;  
Best local Similarity 100.0%; Pred. No. 5.8e-113;  
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGTTGATCGCACTATGACTGTGAAAGATCCCGGCGGAGACACAGTTCCGAAAGC 60  
DB 83 CTGGTTGATCGCACTATGACTGTGAAAGATCCCGGCGGAGACACAGTTCCGAAAGC 142  
QY 61 ACAGCCAGATGAGGAGTCCGGGAAAGGCGTCATGATGTTGCTGTCGCGGACGCT 120  
DB 143 ACAGCCAGATGAGGAGTCCGGGAAAGGCGTCATGATGTTGCTGTCGCGGACGCT 202  
QY 121 CAGGGCTGCTCACTGCGCGGCTCTACAGAGTCAGCCAAAGTCTTGAACGTCGACCCGAC 180  
DB 203 CAGGGCTGCTCACTGCGCGGCTCTACAGAGTCAGCCAAAGTCTTGAACGTCGACCCGAC 262  
QY 181 AATGTGACCTTCTGTGTGCTGCTGCGGTGAGAGAGAGGCGCATTCGCGCTGCAG 240  
DB 263 AATGTGACCTTCTGTGTGCTGCTGCGGTGAGAGAGAGGCGCATTCGCGCTGCAG 322  
QY 241 ATCCATTTTACGCTGATCCAGGCTTCTGCTGCGAGAGACATGACATAGTGCAGTG 300  
DB 323 ATCCATTTTACGCTGATCCAGGCTTCTGCTGCGAGAGACATGACATAGTGCAGTG 382  
QY 301 GGGGATGTGACAGGCTGCGGCTATCTGTGGGCGCGGCGAGAGGCGGGTGCAGCGGC 360

```

|||||
383 GGCATGTGCACGGCTGGCGCTATCGTGGGCGCCGCGAGGAGCGGGTGGCCGGGC 442
361 GACCTGACATGCATCTCTCATTTTGAACCCCAAGAGAGAGCCCTGGAAGATCCCGCTTG 420
443 GACCTGACATGCATCTCTCATTTTGAACCCCAAGAGAGAGCCCTGGAAGATCCCGCTTG 502
421 GAGAGCTCAGCCTGTTTTCGAGAGAGAGCCGAGCGTTAAGCATGCTGGTCCCAATC 480
503 GAGAGCTCAGCCTGTTTTCGAGAGAGAGCCGAGCGTTAAGCATGCTGGTCCCAATC 562
481 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTCTGATGCACTGCTGAGCCCGG 540
563 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTCTGATGCACTGCTGAGCCCGG 622
541 GG 542
623 GG 624

```

LT 3  
9665  
AAA39665 standard; cDNA; 1065 BP.

AAA39665;

18-SRP-2000 (first entry)

Human CR6 cDNA.

CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic;  
immunosuppressive; antimicrobial; therapy; cell proliferation; treatment;  
cell differentiation; cancer; immune disease; rheumatologic disease;  
transplant rejection; anti-infective; CR6; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 98..577  
/tag= a  
/product= "CR6"

US6057427-A.

02-MAY-2000.

05-JUN-1996; 96US-00652446.

20-NOV-1991; 91US-00796066.

10-AUG-1993; 93US-00104736.

27-OCT-1994; 94US-00330108.

05-JUN-1996; 96MO-US008992.

(DART-) DARTMOUTH COLLEGE.

Beadling C, Smith KA;

WPI; 2000-338623/29.

P-PSDB; NAY87957.

Novel antibody or antibody fragment which selectively binds to a

polypeptide encoded by cytokine response gene 2.

Example IV; Col 97-100; 66pp; English.

This invention describes a novel isolated antibody or antibody fragment  
(1) which selectively binds to a polypeptide encoded by cytokine response  
gene 2 (CR2) and modulates CR2 activity. The products of the invention  
have cytostatic, anti-allergic, immunosuppressive and antimicrobial  
activity. The antibodies are useful as therapeutic agents for regulating  
cellular proliferation and differentiation and for treating all kinds of  
cancers, immune diseases such as allergic, autoimmune, and rheumatologic  
diseases, transplant rejection, and as anti-infectives for fighting

CC viral, bacterial, parasitic and fungal infections. This sequence encodes  
CC the human CR6 protein described in the invention  
XX  
SQ Sequence 1065 BP; 198 A; 293 C; 378 G; 196 T; 0 U; 0 Other;

Query Match 98.4%; Score 542; DB 3; Length 1065;  
Best Local Similarity 100.0%; Pred. No. 5.8e-113;  
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CTGTTGATGACATATGACTCTGGAAGAGTCCGCGCCAGAGACACAGTCCGGAAGC 60
DB 83 CTGTTGATGACATATGACTCTGGAAGAGTCCGCGCCAGAGACACAGTCCGGAAGC 142
QY 61 AAGCCAGATGACAGGCTCCGGAAGAGTCCGCGCCAGAGACACAGTCCGGAAGC 120
DB 143 ACAGCCAGATGACAGGCTCCGGAAGAGTCCGCGCCAGAGACACAGTCCGGAAGC 202
QY 121 CAGGCTGCTCAGTCCGCGCCAGAGTCCGCGCCAGAGACACAGTCCGGAAGC 180
DB 203 CAGGCTGCTCAGTCCGCGCCAGAGTCCGCGCCAGAGACACAGTCCGGAAGC 262
QY 181 AATGACCTTCTGTGTGCTGCTGCGGTGAGAGAGACAGGCGACATCCGCTGAG 240
DB 263 AATGACCTTCTGTGTGCTGCTGCGGTGAGAGAGACAGGCGACATCCGCTGAG 322
QY 241 ATCCATTTTACGCTGATCCAGGCTTCTGCTGAGAGAGACATCCGCTGAG 300
DB 323 ATCCATTTTACGCTGATCCAGGCTTCTGCTGAGAGAGACATCCGCTGAG 382
QY 301 GGGATGTGACAGGCGGTGCGGCTATCGTGGGCGCGGAGAGAGCGGCTGCGCGGC 360
DB 383 GGGATGTGACAGGCGGTGCGGCTATCGTGGGCGCGGAGAGAGCGGCTGCGCGGC 442
QY 361 GACCTGACATGATCTCTCATTTTGAACCCCAAGAGAGAGCTGGAAGATCCGCTTG 420
DB 443 GACCTGACATGATCTCTCATTTTGAACCCCAAGAGAGAGCTGGAAGATCCGCTTG 502
QY 421 GAGAGCTCAGCCTGTTTTCGAGAGAGAGCCGAGCGTTAAGCATGCTGGTCCCAATC 480
DB 503 GAGAGCTCAGCCTGTTTTCGAGAGAGAGCCGAGCGTTAAGCATGCTGGTCCCAATC 562
QY 481 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTCTGATGCACTGCTGAGCCCGG 540
DB 563 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTCTGATGCACTGCTGAGCCCGG 622
QY 541 GG 542
DB 623 GG 624

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RESULT 4  
AAA64826  
ID AAA64826 standard; cDNA; 1066 BP.

AAA64826;

20-JUN-2001 (first entry)

Human SYG972 gene coding sequence.

Human; SYG972; cancer diagnosis; cell differentiation; cytostatic;  
breast cancer; lymphoma; Alzheimer's disease; Parkinson's disease;  
degenerative nervous disease; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 98..577  
/tag= a  
/product= "Human SYG972"  
/transl\_except= (pos:269..271,aa:Arg)  
/transl\_except= (pos:299..301,aa:Val)  
/transl\_except= (pos:575..577,aa:Arg)

WO200036147-A1.  
22-JUN-2000.  
09-DEC-1999; 99WO-KR000756.  
12-DEC-1998; 98KR-00054933.  
30-DEC-1998; 98KR-00063958.  
(SAMY-) SAMYANG GENEX CORP.  
Jung N, Kim JM, Yi Y, Bae I, Hong S, Lee H;  
WPI; 2000-431614/37.  
P-PSDB; AAB13772.

Diagnosis of cancer using a probe comprising all or part of an SYG972 gene.

Claim 1, Page 23-24; 31pp; English.

The present sequence is the coding sequence for the human SYG972 gene. SYG972 protein is involved in cell differentiation. SYG972 gene is highly expressed in normal differentiated tissues. However, in cancerous tissues, SYG972 gene expression is inhibited. This characteristic of SYG972 gene expression may be used in cancer diagnosis, especially breast cancer. In addition, the SYG972 gene may be used in distinguishing B cells and T cells in determining the origin of cancer in various lymphomas. SYG972 gene and promoter are useful for designing and screening drugs to promote or inhibit apoptosis and differentiation of cells, especially to screen drugs to treat diseases where cell differentiation and apoptosis occur abnormally e.g. cancer, Alzheimer's disease, Parkinson's disease and degenerative nervous diseases

Sequence 1066 BP; 199 A; 293 C; 378 G; 196 T; 0 U; 0 Other;

100.0%; Score 542; DB 3; Length 1066;  
Local Similarity 100.0%; Pred. No. 5.8e-113;  
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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3 CTGGTGTATGCGACTATGACTGTGAAGAACTCCGGCGGCGAGACAGATTCCGAAAGC 142
4 |||||
5 ACAGCCAGATGCGAGGCGTCCGGGAAAGCGCTCATGATTGCTGTCGCGGCAAGCT 120
6 |||||
7 ACAGCCAGATGCGAGGCGTCCGGGAAAGCGCTCATGATTGCTGTCGCGGCAAGCT 202
8 |||||
9 CAGGGTGGCTCTCATGCGCGGCTCTAGAGTCAAGCCAAAGTCTTGAACCTGGAC 180
10 |||||
11 CAGGGTGGCTCTCATGCGCGGCTCTAGAGTCAAGCCAAAGTCTTGAACCTGGAC 262
12 |||||
13 AATGTACCTTGTGTGCTGCGGCGTGAAGAGACGAGGCGACATCGCGTGCAG 240
14 |||||
15 AATGTACCTTGTGTGCTGCGGCGTGAAGAGACGAGGCGACATCGCGTGCAG 322
16 |||||
17 ATTCATTTTAAAGCTGATCCAGGCTTTTCTGCTGCGAAGACATCGCATATGCGCGTG 300
18 |||||
19 ATTCATTTTAAAGCTGATCCAGGCTTTTCTGCTGCGAAGACATCGCATATGCGCGTG 382
20 |||||
21 GGGGATGTGAGAGGCGTGGCGGCTATCGTGGGCGCGCGAGAGCGGGTGGCGCGGC 360
22 |||||
23 GGGGATGTGAGAGGCGTGGCGGCTATCGTGGGCGCGCGAGAGCGGGTGGCGCGGC 442
24 |||||
25 GACCTGCATCTGATCTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 502
26 |||||
27 GACCTGCATCTGATCTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 582
28 |||||
29 GAGAACTCAGCGCTGTTTTCGAGAGAGCGCGAGCGTTAAGCACTGGGTGCCAGATC 480
30 |||||
31 GAGAACTCAGCGCTGTTTTCGAGAGAGCGCGAGCGTTAAGCACTGGGTGCCAGATC 562
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QY 481 ACCCTCCCCAGATGACAGCGCCCGCGGAGACCTTGGTCTGATGAGCTGTGTGACGCCCGCG 540  
|||  
DB 563 ACCCTCCCCAGATGACAGCGCCCGCGGAGACCTTGGTCTGATGAGCTGTGTGACGCCCGCG 622  
|||  
QY 541 GG 542  
||  
DB 623 GG 624  
||  
RESULT 5  
ADP65476  
ID ADP65476 standard; DNA; 1066 BP.  
XX  
AC ADP65476;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human cytokine responsive protein (CRF) mRNA, complete cds DNA.  
XX  
KW autoimmune disease; arthritis; gene expression analysis;  
KW rheumatoid arthritis; collagen-induced; immunosuppressive; antineumatic;  
KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;  
KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;  
KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
KW immune; ds; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2003072827-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 31-OCT-2002; 2002WO-US035433.  
XX  
PR 31-OCT-2001; 2001US-0336220P.  
XX  
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
XX  
PI Hirsch R, Thornton SL;  
XX  
DR WPI; 2003-712740/67.  
XX  
PT GENBANK; AF079806.  
XX  
PT Diagnosing and analyzing autoimmune disease using gene expression  
PT profiles and microarray technology; useful for diagnosing and treating  
PT rheumatoid arthritis; lupus; fibrositis; osteoarthritis; fibromyalgia and  
PT gout.  
XX  
PS Disclosure; Page; 56pp; English.  
XX  
CC The invention relates to a novel method for diagnosing and analyzing  
CC autoimmune disease or arthritides. The method comprises obtaining a  
CC patient sample containing mRNA, analyzing gene expression using the mRNA  
CC that results in a gene expression signature of the mRNA, and using that  
CC gene expression signature to diagnose or analyse the autoimmune disease  
CC or arthritides in the patient, where gene expression of at least 60% of  
CC the genes correlates with that of the gene signature. The invention  
CC further comprises: a treatment of rheumatoid arthritis; identification of  
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
CC efficacy of a candidate drug in vitro for the treatment of collagen-  
CC induced arthritis; and reducing the symptoms associated with collagen-  
CC induced arthritis. The compositions of the invention have the following  
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
CC antiout, antiinflammatory, dermatological, and immunomodulatory. The  
CC methods and compositions of the present invention are useful for  
CC diagnosing and treating autoimmune disease or arthritides, such as  
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
CC immune disease caused by an infectious agent. This polynucleotide  
CC represents a DNA sequence relating to the genes used in the analysis and

treatment of autoimmune diseases or arthritides. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from WIPO.

Sequence 1066 BP; 199 A; 293 C; 378 G; 196 T; 0 U; 0 Other;

Query Match 98.4%; Score 542; DB 11; Length 1066;  
 Local Similarity 100.0%; Pred. No. 5.8e-113;  
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CTGGTTGATGCACTATGATCTTGGAAAGTCCGCGGCGAGGACACAGTTCCGGAAAGC 60
  |||
83 CTGGTTGATGCACTATGATCTTGGAAAGTCCGCGGCGAGGACACAGTTCCGGAAAGC 142
  |||
61 ACAGCCAGATGAGGAGGCGCGGAAAGCCCTCATGATGCTGCTGCTGCGGCGAGCCT 120
  |||
143 ACAGCCAGATGAGGAGGCGCGGAAAGCCCTCATGATGCTGCTGCTGCGGCGAGCCT 202
  |||
121 CAGGAGTGCCTCACTGCGGCGCTTACAGAGTCAAGCCAAAGCTTTGAACTGACCCGAC 180
  |||
203 CAGGAGTGCCTCACTGCGGCGCTTACAGAGTCAAGCCAAAGCTTTGAACTGACCCGAC 262
  |||
181 AATGTGACCTTCTGTGTGCTGCTGCGGCGTGAAGAGACGAGGCGGACATCGGCTGAC 240
  |||
263 AATGTGACCTTCTGTGTGCTGCTGCGGCGTGAAGAGACGAGGCGGACATCGGCTGAC 322
  |||
241 ATCCATTTTACGCTGATCCAGGCTTCTGCTGCGAAGACATGCAATGATGCGGCTG 300
  |||
323 ATCCATTTTACGCTGATCCAGGCTTCTGCTGCGAAGACATGCAATGATGCGGCTG 382
  |||
301 GGGGATGTGAGCGGCTGCGGCGCTATGCTGCGGCGCGCGGAGAGCGGCTGCGCGGCG 360
  |||
383 GGGGATGTGAGCGGCTGCGGCGCTATGCTGCGGCGCGCGGAGAGCGGCTGCGCGGCG 442
  |||
361 GACCTGACCTGCACTCTCATTTTGGAAACCCAGAGAGACCTGGAAGATCCCGGCTTG 420
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421 GAGAGGCTGACCTGTTTTCGAGAGAGCGGAGCTTAAAGCATGGTGGCCAGATC 480
  |||
503 GAGAGGCTGACCTGTTTTCGAGAGAGCGGAGCTTAAAGCATGGTGGCCAGATC 562
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481 ACCCTCCCGAGTGAAGCCCGGCGGAGCTTGTGTATGCACTGTGTGAGCGCCCGG 540
  |||
563 ACCCTCCCGAGTGAAGCCCGGCGGAGCTTGTGTATGCACTGTGTGAGCGCCCGG 622
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541 GG 542
  ||
623 GG 624
  
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LT 6  
 9049  
 ACC59049 standard; DNA; 1078 BP.  
 ACC59049;

03-JUL-2003 (first entry)

Human Gadd45 gene SEQ ID NO: 9.

Human; c-Jun-N-terminal kinase pathway; JNK pathway; cytosolic;  
 programmed cell death; TNFalpha; Fas; TRAIL; genotoxic agent; cancer;  
 apoptosis; Gadd45beta; JNK2; chronic inflammatory disease; Gadd45;  
 autoimmune condition; gene; ds.

Homo sapiens.  
 WO2003028659-A2.

10-APR-2003.

02-OCT-2002; 2002WO-US031548.

XX 02-OCT-2001; 2001US-0326492P.  
 PR 12-OCT-2001; 2001US-0328811P.  
 XX  
 XX  
 PA (UYCH-) UNIV CHICAGO.  
 PI Franzoso G, De Smaele E, Zazzaroni F, Papa S;  
 DR WPI; 2003-430155/40.  
 DR P-PSDB; ABR40340.  
 PT Modulating pathways leading to programmed cell death, by selecting a  
 target within Jun-N-terminal kinase pathway and interfering with the  
 target using agent that up or down regulates the JNK pathway.  
 PT  
 PS Disclosure; Page 122; 131pp; English.

CC The invention relates to a novel method for modulating pathways leading  
 CC to programmed cell death, comprising selecting a target within the c-Jun-  
 CC N-terminal kinase (JNK) pathway, and interfering with the target using  
 CC an agent that either up regulates or down regulates the JNK pathway. The  
 CC method of the invention has cytosolic activity. A method of the  
 CC invention is useful for modulating pathways leading to programmed cell  
 CC death induced by TNFalpha, Fas, TRAIL, genotoxic agent such as  
 CC doxorubicin or cisplatin. Another method of the invention is useful  
 CC for screening and identifying an agent, preferably peptides, peptide  
 CC mimetics, peptide-like molecules, mutant proteins, cDNAs, antisense  
 CC oligonucleotides or constructs, lipids, carbohydrates or synthetic or  
 CC natural chemical compounds, that modulate JNK pathway in vitro. A method  
 CC of the invention may also be useful for treating cancer, and for  
 CC preventing apoptosis. Compounds that are capable of interfering with the  
 CC ability of Gadd45beta to associate with JNK2 are useful for treating  
 CC human diseases such as chronic inflammatory, and autoimmune conditions  
 CC and certain types of cancer. The present sequence is used in the  
 CC exemplification of the invention

SQ Sequence 1078 BP; 200 A; 297 C; 382 G; 199 T; 0 U; 0 Other;

Query Match 98.4%; Score 542; DB 8; Length 1078;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-113;  
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 95 CTGGTTGATGCACTATGATCTTGGAAAGTCCGCGGCGAGGACACAGTTCCGGAAAGC 154
  |||
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DB 155 ACAGCCAGATGAGGAGGCGCGGAAAGCCCTCATGATGCTGCTGCTGCGGCGAGCCT 214
  |||
QY 121 CAGGAGTGCCTCACTGCGGCGCTTACAGAGTCAAGCCAAAGCTTTGAACTGACCCGAC 180
  |||
DB 215 CAGGAGTGCCTCACTGCGGCGCTTACAGAGTCAAGCCAAAGCTTTGAACTGACCCGAC 274
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DB 275 AATGTGACCTTCTGTGTGCTGCTGCGGCGTGAAGAGACGAGGCGGACATCGGCTGAC 334
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QY 241 ATCCATTTTACGCTGATCCAGGCTTCTGCTGCGAAGACATGCAATGATGCGGCTG 300
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DB 335 ATCCATTTTACGCTGATCCAGGCTTCTGCTGCGAAGACATGCAATGATGCGGCTG 394
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DB 395 GGGGATGTGAGCGGCTGCGGCGCTATGCTGCGGCGCGGAGAGAGCGGCTGCGCGGCG 454
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DB 455 GACCTGACCTGCACTCTCATTTTGGAAACCCAGAGAGCGCTGGAAGATCCCGGCTTG 514
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QY 421 GAGAGGCTGACCTGTTTTCGAGAGAGCGGAGCTTAAAGCATGGTGGCCAGATC 480
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DB 515 GAGAGGCTGACCTGTTTTCGAGAGAGCGGAGCTTAAAGCATGGTGGCCAGATC 574
  |||
  
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541 GG 542  
 635 GG 636

T 7  
 1003  
 ADP65003 standard; DNA; 1078 BP.

ADP65003;

12-AUG-2004 (first entry)

Human growth arrest and-damage-inducible, gamma DNA sequence.

autoimmune disease; arthritis; gene expression analysis;  
 rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;  
 antiarthritis; osteopathic; antignout; antiinflammatory; dermatological;  
 immunomodulatory; lupus; ankylosing spondylitis; fibrositis;  
 fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
 immune; ds; human.

Homo sapiens.

WO2003072827-A1.

04-SEP-2003.

31-OCT-2002; 2002WO-US035433.

31-OCT-2001; 2001US-0336220P.

(CHILD-) CHILDREN'S HOSPITAL MEDICAL CENT.

Hirsch R, Thornton SL;

WPI: 2003-712740/67.

GENBANK; NM\_006705.

Diagnosing and analyzing autoimmune disease using gene expression  
 profiles and microarray technology, useful for diagnosing and treating  
 rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 gout.

Disclosure; Page; 56pp; English.

The invention relates to a novel method for diagnosing and analyzing  
 autoimmune disease or arthritides. The method comprises obtaining a  
 patient sample containing mRNA, analysing gene expression using the mRNA  
 that results in a gene expression signature of the mRNA, and using that  
 gene expression signature to diagnose or analyse the autoimmune disease  
 or arthritides in the patient, where gene expression of at least 60% of  
 the genes correlates with that of the gene signature. The invention  
 further comprises a treatment of rheumatoid arthritis; identification of  
 genes for targeting in the treatment of rheumatoid arthritis in a mammal;  
 other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 analysis of autoimmune disease or rheumatoid arthritis; screening the  
 efficacy of a candidate drug in vitro for the treatment of collagen-  
 induced arthritis; and reducing the symptoms associated with collagen-  
 induced arthritis. The compositions of the invention have the following  
 activities: immunosuppressive, antirheumatic, antiarthritis, osteopathic,  
 antignout, antiinflammatory, dermatological, and immunomodulatory. The  
 methods and compositions of the present invention are useful for  
 diagnosing and treating autoimmune disease or arthritides, such as  
 rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 immune disease caused by an infectious agent. This polynucleotide

CC represents a DNA sequence relating to the genes used in the analysis and  
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
 CC not shown in the specification. It has been supplied in an electronic  
 CC format from WIPO.

XX Sequence 1078 BP; 200 A; 297 C; 382 G; 199 T; 0 U; 0 Other;

Query Match 98.4%; Score 542; DB 11; Length 1078;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-113;  
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CTGATTGATCGCATTGACCTCTGGAAGAAGTCCGCGCAGACACAGTTCCGAAAAC	60
DB	95	CTGATTGATCGCATTGACCTCTGGAAGAAGTCCGCGCAGACACAGTTCCGAAAAC	154
QY	61	ACAGCCAGAGATCAGAGGTGCGGAAAGCGCTGATGATTGCTGTCGCGCAGCGT	120
DB	155	ACAGCCAGAGATCAGAGGTGCGGAAAGCGCTGATGATTGCTGTCGCGCAGCGT	214
QY	121	CAGGCTGCTCTACCTGCGGCGCTTACAGATGACCAAGTCTTGAAGTGAACCCGAC	180
DB	215	CAGGCTGCTCTACCTGCGGCGCTTACAGATGACCAAGTCTTGAAGTGAACCCGAC	274
QY	181	AATGTGACCTTCTGTGTGCTGCTGCGGCTGAGAGACGAGGCGACATCCGCTGCAG	240
DB	275	AATGTGACCTTCTGTGTGCTGCTGCGGCTGAGAGACGAGGCGACATCCGCTGCAG	334
QY	241	ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAAGACGACATGATGCGCGTG	300
DB	335	ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAAGACGACATGATGCGCGTG	394
QY	301	GGCGATGTCAGACGGCTGCGGCTTATCGTGGCGCGCGGAGAGGCGGCTGCGCGGC	360
DB	395	GGCGATGTCAGACGGCTGCGGCTTATCGTGGCGCGCGGAGAGGCGGCTGCGCGGC	454
QY	361	GACCTGCACTGATCTCTATTTCGAACCCCAAGAGAGCGCTGAGAGATCCGCTTG	420
DB	455	GACCTGCACTGATCTCTATTTCGAACCCCAAGAGAGCGCTGAGAGATCCGCTTG	514
QY	421	GAGAACTCAGCTGTTTTCGAGAGAGCGGCAAGCTTATGAGTGGTCCGACATC	480
DB	515	GAGAACTCAGCTGTTTTCGAGAGAGCGGCAAGCTTATGAGTGGTCCGACATC	574
QY	481	ACCCTCCCGAGTACACGCCCGCGGACCTTGTCTGATGAGTGGTGAAGCCCGG	540
DB	575	ACCCTCCCGAGTACACGCCCGCGGACCTTGTCTGATGAGTGGTGAAGCCCGG	634
QY	541	GG 542	
DB	635	GG 636	

RESULT 8  
 ADJ74785  
 ID ADJ74785 standard; DNA; 1078 BP.  
 XX ADJ74785;  
 XX 20-MAY-2004 (first entry)  
 XX Marker gene SEQ ID NO:37.  
 XX  
 XX bronchial asthma; chronic obstructive pulmonary disease;  
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
 KW gene therapy; marker gene; gene; ds.  
 XX  
 XX Homo sapiens.  
 XX  
 XX EPI394274-A2.  
 XX  
 XX 03-MAR-2004.  
 XX  
 XX 04-AUG-2003; 2003EP-00254857.



06-AUG-2002; 2002JP-00229312.  
20-MAR-2003; 2003JP-00077212.

(GENO-) GENOX RES INC.

Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;

WPI; 2004-193155/19.

Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.

Claim 1; SEQ ID NO 37; 241bp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antisthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

Sequence 1078 BP; 200 A; 297 C; 382 G; 199 T; 0 U; 0 Other;

ery March 98.4%; Score 542; DB 12; Length 1078;  
st Local Similarity 100.0%; Pred. No. 5.8e-113; Indels 0; Gaps 0;  
tches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGTTGATCGCACTATGACTCTGGAAGATCCGCGCCGAGACACATGTTCCGAAAGC 60  
CTGTTGATCGCACTATGACTCTGGAAGATCCGCGCCGAGACACATGTTCCGAAAGC 154  
95  
61 ACAGCCAGATGACAGGAGCGCGGAAAGCGTGCATGATGTTGCTGGGCGACAGGT 120  
155 ACAGCCAGATGACAGGAGCGCGGAAAGCGTGCATGATGTTGCTGGGCGACAGGT 214  
121 CAGGCGTCCCTCAGCTGCGGCGGTCTACAGATCAGCAAAAGTCTTGAACGTGAGCCCGAC 180  
215 CAGGCGTCCCTCAGCTGCGGCGGTCTACAGATCAGCAAAAGTCTTGAACGTGAGCCCGAC 274  
181 AATGTACCTTCTGTGTGCTGCGGCTGAGAGAGACGAGGCGACATGCGCTGAG 240  
275 AATGTACCTTCTGTGTGCTGCGGCTGAGAGAGACGAGGCGACATGCGCTGAG 334  
241 ATCAATTTTACGCTGATCAGAGCTTTCGCTGCGAGAACGACATGACATAGTGGCGCTG 300  
335 ATCAATTTTACGCTGATCAGAGCTTTCGCTGCGAGAACGACATGACATAGTGGCGCTG 394

QY 301 GCGATGTGACACGCGCTGCGGCTATCTGTTGGGCGCGCGAGAGGCGGCGCGGCG 360  
DB 395 GCGATGTGACACGCGCTGCGGCTATCTGTTGGGCGCGCGAGAGGCGGCGCGGCG 454  
QY 361 GACCTGCACTGATCCTCATTTTGAACCCCAACGAGAGCGCTGGAAGATCCGCGCTTG 420  
DB 455 GACCTGCACTGATCCTCATTTTGAACCCCAACGAGAGCGCTGGAAGATCCGCGCTTG 514  
QY 421 GAGAGCTCAGCCTGTTTTCGAGAGAGACCCGACGCTTAAAGCATGCTGGTCCACATC 480  
DB 515 GAGAGCTCAGCCTGTTTTCGAGAGAGACCCGACGCTTAAAGCATGCTGGTCCACATC 574  
QY 481 ACCCTCCCGAGTGAAGCGCGCGGAGACCTTGTCTAGTGAAGTGAAGCGCGCGG 540  
DB 575 ACCCTCCCGAGTGAAGCGCGCGGAGACCTTGTCTAGTGAAGTGAAGCGCGCGG 634  
QY 541 GG 542  
DB 635 GG 636

#### RESULT 9

ADR25449 standard; DNA; 1078 BP.

ADR25449;

21-OCT-2004 (first entry)

Breast cancer prognosis marker #1310.

de; breast cancer; prognosis; gene expression; diagnosis.

OS Homo sapiens.

PN W02004065545-A2.

XX 05-AUG-2004.

PF 15-JAN-2004; 2004MO-US001100.

PR 15-JAN-2003; 2003JUS-00342887.

PA (ROSE-) ROSETTA INPHARMATICS LLC.

PI (NECA-) NETHERLANDS CANCER INST.

Van't Veer LJ, He Y;

WPI; 2004-593473/57.

Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.

Disclosure; SEQ ID NO 1310; 226bp; English.

The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.

Sequence 1078 BP; 200 A; 297 C; 382 G; 199 T; 0 U; 0 Other;

Query Match 98.4%; Score 542; DB 13; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 5.8e-113;  
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGGCCAGGACACAGTTCCGGAAAGC 60  
XX |||||  
XX |||||  
DR CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGGCCAGGACACAGTTCCGGAAAGC 154  
P-PSDB; ADX85166.  
61 ACAGCCAGGATGCAAGGGTCCGGGAAAGCGCTGCAAGATGTTGCTGTCCGGCCAGCGT 120  
XX |||||  
XX |||||  
PT ACAGCCAGGATGCAAGGGTCCGGGAAAGCGCTGCAAGATGTTGCTGTCCGGCCAGCGT 214  
PT |||||  
PT |||||  
121 CAGGGCTGCTCACTCCGGCGCTCTACAGAGTCAGGCCAAGTCTTGAACGTGACCCCGAC 180  
XX |||||  
XX |||||  
PS CAGGGCTGCTCACTCCGGCGCTCTACAGAGTCAGGCCAAGTCTTGAACGTGACCCCGAC 274  
XX |||||  
XX |||||  
181 AATGTACCTTCTGTGTGCTGCTGGGGTGAAGAGAGGAGGCGACATCCGCGTGCAG 240  
XX |||||  
XX |||||  
275 AATGTACCTTCTGTGTGCTGCTGGGGTGAAGAGAGGAGGCGACATCCGCGTGCAG 334  
XX |||||  
XX |||||  
241 ATCCATTTTAAAGCTGATCCAGGCTTTCTGCTGCGAAGACGACATCGACATAGTCCGCTG 300  
XX |||||  
XX |||||  
335 ATCCATTTTAAAGCTGATCCAGGCTTTCTGCTGCGAAGACGACATCGACATAGTCCGCTG 394  
XX |||||  
XX |||||  
301 GGGGATGTGCAAGCGCTGGCGGCTATCTGTGGCGCGCGCGAGAGGCGGGTGCAGCGGC 360  
XX |||||  
XX |||||  
395 GGGGATGTGCAAGCGCTGGCGGCTATCTGTGGCGCGCGCGAGAGGCGGGTGCAGCGGC 454  
XX |||||  
XX |||||  
361 GACCTGCACTGCACTCTCTCAATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 420  
XX |||||  
XX |||||  
455 GACCTGCACTGCACTCTCTCAATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 514  
XX |||||  
XX |||||  
421 GAGAACTCAGCCTGTTTTGCGAGAGAGCGCAGCGCTTAAAGTCTGGTCCCAAGATC 480  
XX |||||  
XX |||||  
515 GAGAACTCAGCCTGTTTTGCGAGAGAGCGCAGCGCTTAAAGTCTGGTCCCAAGATC 574  
XX |||||  
XX |||||  
481 ACCCTCCCGAGTGAAGACCCCGCGGGAGACTTGTGTGATGACAGTGTGATGACCCCGG 540  
XX |||||  
XX |||||  
575 ACCCTCCCGAGTGAAGACCCCGCGGGAGACTTGTGTGATGACAGTGTGATGACCCCGG 634  
XX |||||  
XX |||||  
541 GG 542  
635 GG 636

.T 10  
.165  
ADX85165 standard; DNA; 1078 BP.

ADX85165;

05-MAY-2005 (first entry)

Human gadd45 DNA, seqid:9.

Cell death; apoptosis; degeneration; cancer; cytostatic; neoplasm;  
immunotherapy; chemotherapy; gene therapy; gadd45;  
Jun N terminal kinase modulator; gene; ds.

Homo sapiens.

Key Location/Qualifiers  
CDS 110..589  
/\*tag= a  
/product= "Human gadd45 protein"

EP1506784-A1.

16-FEB-2005.

26-JUL-2004; 2004BP-00017667.

25-JUL-2003; 2003US-00626905.  
02-DEC-2003; 2003US-0526231P.

(UYCH-) UNIV CHICAGO.

PI Franzoso G, Desmaele E, Zazzeroni F, Papa S, Bubicl C;  
XX WPI; 2005-154742/17.  
XX DR P-PSDB; ADX85166.  
XX Method for modulating pathways leading to programmed cell death for  
XX treating cancer, by obtaining peptide having specific amino acid sequence  
XX PT and regulating JNK pathway using peptide or composition developed using  
XX PT peptide sequence.  
XX Example 14; SEQ ID NO 9; 110pp; English.  
XX  
XX The invention relates to methods and compositions for modulating pathways  
XX leading to programmed cell death or apoptosis. The method involves  
XX selecting a target within the c-Jun-N-terminal kinase (JNK) pathway and  
XX interfering the target by an agent that either upregulates or  
XX downregulates the JNK pathway. The JNK modulator is effective in treating  
XX degenerative disease and cancer. The method and compositions of the  
XX invention are useful in immunotherapy, cancer chemotherapy and in gene  
XX therapy. The present sequence is the human gadd45 DNA which is a  
XX modulator of JNK pathway.

Sequence 1078 BP; 200 A; 297 C; 382 G; 199 T; 0 U; 0 Other;

Query Match 98.4%; Score 542; DB 14; Length 1078;  
Best Local Similarity 100.0%; Pred. No. 5.8e-113;  
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGGCCAGGACACAGTTCCGGAAAGC 60  
DB 95 CTGGTTGATCGCACTATGACTCTGGAAGAAGTCCGGCCAGGACACAGTTCCGGAAAGC 154  
QY 61 ACAGCCAGGATGCAAGGGTCCGGGAAAGCGCTGCAAGATGTTGCTGTCCGGCCAGCGT 120  
DB 155 ACAGCCAGGATGCAAGGGTCCGGGAAAGCGCTGCAAGATGTTGCTGTCCGGCCAGCGT 214  
QY 121 CAGGGCTGCTCACTCCGGCGCTCTACAGAGTCAGGCCAAGTCTTGAACGTGACCCCGAC 180  
DB 215 CAGGGCTGCTCACTCCGGCGCTCTACAGAGTCAGGCCAAGTCTTGAACGTGACCCCGAC 274  
QY 181 AATGTACCTTCTGTGTGCTGCTGGGGTGAAGAGAGGAGGCGACATCCGCGTGCAG 240  
DB 275 AATGTACCTTCTGTGTGCTGCTGGGGTGAAGAGAGGAGGCGACATCCGCGTGCAG 334  
QY 241 ATCCATTTTAAAGCTGATCCAGGCTTTCTGCTGCGAAGACGACATGATGACCGCTG 300  
DB 335 ATCCATTTTAAAGCTGATCCAGGCTTTCTGCTGCGAAGACGACATGATGACCGCTG 394  
QY 301 GGGGATGTGCAAGCGCTGGCGGCTATCTGTGGCGCGCGAGAGGCGGGTGCAGCGGC 360  
DB 395 GGGGATGTGCAAGCGCTGGCGGCTATCTGTGGCGCGCGAGAGGCGGGTGCAGCGGC 454  
QY 361 GACCTGCACTGCACTCTCTCAATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 420  
DB 455 GACCTGCACTGCACTCTCTCAATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 514  
QY 421 GAGAACTCAGCCTGTTTTGCGAGAGAGCGCAGCGCTTAAAGTCTGGTCCCAAGATC 480  
DB 515 GAGAACTCAGCCTGTTTTGCGAGAGAGCGCAGCGCTTAAAGTCTGGTCCCAAGATC 574  
QY 481 ACCCTCCCGAGTGAAGACCCCGCGGGAGACTTGTGTGATGACAGTGTGATGACCCCGG 540  
DB 575 ACCCTCCCGAGTGAAGACCCCGCGGGAGACTTGTGTGATGACAGTGTGATGACCCCGG 634  
QY 541 GG 542  
DB 635 GG 636

RESULT 11  
AAT74048  
ID AAT74048 standard; cDNA; 1036 BP.  
XX

AA174048;

17-FEB-1998 (first entry)

Human GRP17 cDNA clone GEN-554H06.

GRP17 gene; Gadd45 and MyD118 related protein; human; cell growth arrest; DNA damage; cancer; autoimmune disease; diagnosis; therapy; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	84..563
	/*tag= a
polyA_signal	1020..1025
	/*tag= b

EP787798-A2.

06-AUG-1997.

10-FEB-1997; 97EP-00102108.

09-FEB-1996; 96JP-00023612.

(SAXA ) OTSUKA PHARM CO LTD.

Suzuki M, Watanabe T, Fujiwara T;

WPI; 1997-387484/36.

P-PSDB; AAW23533.

New GRP17 gene associated with arrest of cell growth and induction of DNA damage - useful for diagnosis and treatment of cancer, auto-immune diseases etc., also for drug screening.

Claim 3; Page 9-10; 12pp; English.

CDNA clone GEN-554H06, which includes a separately claimed coding region (see AA174047), corresponds to a novel gene, designated as human GRP17 (Gadd45 and MyD118 related protein, 17 kDa), that is associated with arrest of cell growth and DNA damage induction. It encodes a protein (see AAW23533) that is highly homologous to proteins encoded by gadd45 and MyD118 genes, both of which are tumour suppressors. The gene maps to chromosome 9q22.1-22.2. GEN-55H06 was isolated from a human placental CDNA library on the basis of homology with gadd45 and MyD118. It is thought that the gene, when it is abnormal, may possibly induce cancer or malformation, and that it may be applied clinically in the diagnosis and/or treatment of cancer, malformation and autoimmune diseases, as well as for screening drugs for treatment of these conditions

Sequence 1036 BP; 183 A; 290 C; 371 G; 192 T; 0 U; 0 Other;

ery Match	97.5%; Score 537.2; DB 2; Length 1036;
st Local Similarity	99.4%; Pred. No. 7e-112;
ches 539; Conservative	0; Mismatches 3; Indels 0; Gaps 0;

```

1 CTGGTGTATGCGCACTATGACTCTGGAAGAGTCCGCGGCGAGACAGATTCCGGAAAGC 60
69 CTGTTGATGACACTATGACTCTGGAAGAGTCCGCGGCGAGACAGATTCCGGAAAGC 128
61 ACAGCCAGATGAGGAGTCCGCGGAAAGCCCTGCATGATTGCTGCTGCGGCGACGCT 120
129 ACAGCCAGATGAGGAGTCCGCGGAAAGCCCTGCATGATTGCTGCTGCGGCGACGCT 188
121 CAGGCGTCCCTCACTGCGCGGCTTTACAGTCAAGCTTTGAACGTTGACATCCCGAC 180
189 CAGGCGTCCCTCACTGCGCGGCTTTACAGTCAAGCTTTGAACGTTGACATCCCGAC 248
181 AATGTGACCTTGTGTGTGCTGCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
249 AATGTGACCTTGTGTGTGCTGCGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 308

```

```

QY 241 ATCCATTTTACGCTGATCCAGGCTTTTGTGCTGCCGAGAACATGACATAGTGGCGGCG 300
DB 309 ATCCATTTTACGCTGATCCAGGCTTTTGTGCTGCCGAGAACATGACATAGTGGCGGCG 368
QY 301 GGGCGATGTGACAGCGGCTGGCGGCTATCGTGGGCGCGGCGAGAGAGCGGCGTGGCG 360
DB 369 GGGCGATGTGACAGCGGCTGGCGGCTATCGTGGGCGCGGCGAGAGAGCGGCGTGGCG 428
QY 361 GACCTGCACTGATCCTCATTTTGAACCCCAACGAGAGCGCTGGAAGATCCCGCTTGG 420
DB 429 GACCTGCACTGATCCTCATTTTGAACCCCAACGAGAGCGCTGGAAGATCCCGCTTGG 488
QY 421 GAGAACTTCAAGCTGTTTGGAGAGAGAGCGGCGAGAGAGCGGCGTGAAGATCCCGCATC 480
DB 489 GAGAACTTCAAGCTGTTTGGAGAGAGAGCGGCGAGAGAGCGGCGTGAAGATCCCGCATC 548
QY 481 ACCCTCCCGAGTGAAGCGCGGCGGAGCTTGTGTGATGAGTGTGAGCGCCCGG 540
DB 549 ACCCTCCCGAGTGAAGCGCGGCGGAGCTTGTGTGATGAGTGTGAGCGCCCGG 608
QY 541 GG 542
DB 609 GG 610

RESULT 12
AD131494
ID AD131494 standard; cDNA; 750 BP.
XX
AC AD131494;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human cDNA #820.
XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypersplenophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukemia; anti-inflammatory; antiaesthetic; anticancer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
OS Homo sapiens.
XX
PN US6607879-B1.
XX
PD 19-AUG-2003.
XX
PF 09-FEB-1998; 98US-00023655.
XX
PR 09-FEB-1998; 98US-00023655.
XX
PA (INCY-) INCYTE CORP.
XX
PI Cocks BG, Stuart SG, Selhammer JD;
XX
DR WPI; 2003-895307/82.
XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.
XX
PS Claim 1; SEQ ID NO 820; 50pp; English.
XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected

```



|||||  
 384 GGGGATGTGACAGCGCTGGCGCTATCGTGGCGCCGCGAGAGCGGGTGGCCGCGC 443  
 361 GACCTGACATGCTCTCTCATTTTGAACCCCAAGAGAGCGCTT-GGAGAGATCCGCTT 419  
 444 GACCTGACATGCTCTCTCATTTTGAACCCCAAGAGAGCGCTTGGAGAGATCCGCTT 503  
 420 GGAGAGCTCAGCTCTGTTTTCGAGAGAGAGCCGAGCGTTACGACTGGGTGCCAGCAT 479  
 504 GGAGAGCTCAGCTCTGTTTTCGAGAGAGAGCCGAGCGTTACGACTGGGTGCCAGCAT 563  
 480 CACCTTCCCGAGTGAAGCCGCGGAGCTTGGTCTGATGAGTGTGACGCGCCG 539  
 564 CACCTTCCCGAGTGAAGCCGCGGAGCTTGGTCTGATGAGTGTGACGCGCCG 623  
 540 GGG 542  
 624 GGG 626

L/T 14  
 0819

ADQ20819 standard; DNA; 612 BP.

ADQ20819;

26-AUG-2004 (first entry)

Human soft tissue sarcoma-upregulated DNA - SEQ ID 3639.

soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human; ds.

Homo sapiens.

WO2004048938-A2.

10-JUN-2004.

26-NOV-2003; 2003WO-US038193.

26-NOV-2002; 2002US-0429739P.

(PROT-) PROTEIN DESIGN LABS INC.

Aziz N, Ginsburg WM, Zlotnik A;

WPI; 2004-441208/41.

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

Example 2; SEQ ID NO 3639; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytoskeletal applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 612 BP; 108 A; 181 C; 208 G; 115 T; 0 U; 0 Other;

Entry Match

95.4%; Score 525.4; DB 12; Length 612;

Best Local Similarity 99.8%; Pred. No. 3e-109; Matches 526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGTTGATGCACTATGACTCTGAGAGAAAGTCCGGGCGAGACACAGTCCGAAAGC 60  
 Db 86 CTGTTGATGCACTATGACTCTGAGAGAAAGTCCGGGCGAGACACAGTCCGAAAGC 145  
 QY 61 ACAGCCAGGATGCAAGGATGCGGGAAGCGCTGCAATGACTTGTGTCGGGCGAGCCT 120  
 Db 146 ACAGCCAGGATGCAAGGATGCGGGAAGCGCTGCAATGACTTGTGTCGGGCGAGCCT 205  
 QY 121 CAGGGGTGCTCACTGCGGCGCTCTACAGAGTCAAGCAAGTCTTGAAGTGAACCCGAC 180  
 Db 206 CAGGGGTGCTCACTGCGGCGCTCTACAGAGTCAAGCAAGTCTTGAAGTGAACCCGAC 265  
 QY 181 AATGTGACCTTCTGTGTGCTGCTGCGGCTGAGAGAGACGAGGCGCATCATGCTGTCAG 240  
 Db 266 AATGTGACCTTCTGTGTGCTGCTGCGGCTGAGAGAGACGAGGCGCATCATGCTGTCAG 325  
 QY 241 ATTCATTTTACGCTGATTCAGAGCTTTCTGCTGAGAGACGACATTCGACATGTCGCGCTG 300  
 Db 326 ATTCATTTTACGCTGATTCAGAGCTTTCTGCTGAGAGACGACATTCGACATGTCGCGCTG 385  
 QY 301 GGGGATGTGACAGCGGCTGGGCGCTATCGTGGGCGCGCGAGAGCGGGTGGCGCGGCG 360  
 Db 386 GGGGATGTGACAGCGGCTGGGCGCTATCGTGGGCGCGCGAGAGCGGGTGGCGCGGCG 445  
 QY 361 GACCTGACATGCTCTCTCATTTTGAACCCCAAGAGAGCGCTTGAAGATCCGCTTG 420  
 Db 446 GACCTGACATGCTCTCTCATTTTGAACCCCAAGAGAGCGCTTGAAGATCCGCTTG 505  
 QY 421 GAGAGCTCAGCTCTGTTTTCGAGAGAGAGCCGAGCGTTACGACTGGGTGCCAGATC 480  
 Db 506 GAGAGCTCAGCTCTGTTTTCGAGAGAGAGCCGAGCGTTACGACTGGGTGCCAGATC 565  
 QY 481 ACCCTCCCGAGTGAAGAGCCGCGGAGCCTTGTGATGACAGT 527  
 Db 566 ACCCTCCCGAGTGAAGAGCCGCGGAGCCTTGTGATGACAGT 612

RESULT 15

ADQ24782 standard; DNA; 1202 BP.

ADQ24782;

26-AUG-2004 (first entry)

Human soft tissue sarcoma-upregulated DNA - SEQ ID 7602.

soft tissue sarcoma; cytoskeletal; gene therapy; vaccine; screening; human; ds.

Homo sapiens.

WO2004048938-A2.

10-JUN-2004.

26-NOV-2003; 2003WO-US038193.

26-NOV-2002; 2002US-0429739P.

(PROT-) PROTEIN DESIGN LABS INC.

Aziz N, Ginsburg WM, Zlotnik A;

WPI; 2004-441208/41.

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue sarcoma.

Example 2; SEQ ID NO 7602; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cyrostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.

Sequence 1202 BP; 226 A; 314 C; 416 G; 220 T; 0 U; 26 Other;

try Match 93.1%; Score 512.8; DB 12; Length 1202;

ic Local Similarity 94.8%; Pred. No. 2.4e-106;

ches 514; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
Size-selected on agarose gel. Average insert size ~1kb. 5',  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permutt Lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

ry Match 98.4%; Score 542; DB 3; Length 596;  
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE  
AUTHORS  
Hominidae; Homo.  
1 (baes 1 to 637)  
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
Lemshak, I., Scaer, M., Brestelli, J., Gadowohl, G., Clifton, S.,  
Hiller, L., Merra, M., Page, D., Wylie, T., Martin, J., Blaisdell, A.,  
Schmitt, A., Reising, B., Ritter, E., Ronko, I., Bennett, J.,  
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R.,  
Williams, T., Jackson, Y. and Bowers, Y.  
Endocrine Pancreas Consortium  
Unpublished (2000)  
Other ESTs: Ipl1409.x1  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biohp.harvard.edu

TITLE  
JOURNAL  
COMMENT  
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
Washington University Genome Sequencing Center For information on  
obtaining a clone please contact: Dr. Hiroshi Inoue  
(hinoue@im.wustl.edu)  
Seq primer: -40RP from Gibco  
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Location/Qualifiers

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Size-selected on agarose gel. Average insert size ~1kb. 5',  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permutt Lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

# ORIGIN

Query Match 98.4%; Score 542; DB 4; Length 637;  
Best Local Similarity 100.0%; Pred. No. 7.5e-120;  
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Homiidae; Homo.  
 1 (bases 1 to 661)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
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RY Match 98.4%; Score 542; DB 2; Length 661;  
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 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ARCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
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N  
ry Match 98.4%; Score 542; DB 7; Length 727;  
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Homidae; Homo.  
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HORS National Institutes of Health, Mammalian Gene Collection (MGC)  
LE Published (1999)  
RNAL Contact: Robert Strausberg, Ph.D.  
NT Email: cgabs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
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adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 98.4%; Score 542; DB 7; Length 730;  
Best Local Similarity 100.0%; Pred. No. 7.6e-120;  
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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us-10-089-641-1.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	:					
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	:					
Hominidae; Homo.	:					
1 (bases 1 to 1031)	:					
Li W.B., Gruber,C., Jesse,J. and Polajec,D.	:					
Full-length cDNA libraries and normalization	:					
Unpublished	:					
Contact : Feng Liang Email : fliang@lifetech.com URL :	:					
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600	:					
Faraday Avenue	:					
2 (bases 1 to 1031)	:					
Genoscope.	:					
DIRECT Submission	:					
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :	:					
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- Web : www.genoscope.cns.fr)	:					
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primes	:					
end enriched, double-strand cDNA was digested with Not I and cloned	:					
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library	:					
was normalized. Library was constructed by Life Technologies, a	:					
division of Invitrogen.	:					
location/Qualifiers	:					
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/plasmid="pCMVSPORT_6"	:					
IN	:					
try Match	:					
t Local Similarity	:					
ches 542;	:					
Conservative	:					
0;	:					
Mismatches	:					
0;	:					
Indels	:					
0;	:					
Gaps	:					
0;	:					
Score 542;	:					
DB 6;	:					
Length 1031;	:					
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152	:					
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212	:					
CAGGCTGCTCACTGCTGCGCGCTGTACAGATCACGCCAAGCTTGAACGTGACCCCGAC	:					
271	:					
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240	:					
AATGTGACCTTCTGTGTGTGCTGTGCGCGGTGAAGAGACAGAGGCGCAATCCGCGTCAG	:					
331	:					
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300	:					
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391	:					
ATCATTTTAAGCGTATCCAGAGCTTCTGTGCGAAGACATGACATATGAGGCGGTG	:					
360	:					
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451	:					
GGCGATGTGACGCGGCTGCGCGCTATGTGTGCGCGCGCGACAGAGGCGGCTGCGCGGC	:					
420	:					
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511	:					
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[illegible]

	241	ATCCATTTTAGCTGATCATCGAGCTTTCGTGCACGAAGAACAATCAATGATGTCGGTG	300
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	301	GCGCAGTGTGCACGGCTGCGGGCTATCTGTGGCGCGCGGCGAAGAGCGGATGCCCGGCG	360
	377	GCGCAGTGTGCACGGCTGCGGGCTATCTGTGGCGCGCGGCGAAGAGCGGATGCCCGGCG	436
	361	GACCTGCACACTGATCTCTATTTCCAAACCCCAAAGAGACGCTGGAAGATCCGCGCTTG	420
	437	GACCTGCACACTGATCTCTATTTCCAAACCCCAAAGAGACGCTGGAAGATCCGCGCTTG	496
	421	GAGAAGCTCAGCGCTGTTTTGCGAGAGAGACGCGACGCTTTAACGACTGGATGCCAGATC	480
	497	GAGAAGCTCAGCGCTGTTTTGCGAGAGAGACGCGACGCTTTAACGACTGGATGCCAGATC	556
	481	ACCCTTCCCCGAGTGCACAGCCCGCGGGGAACTTGTGTTGATGCAGTGTGACGCCCGCG	540
	557	ACCCTTCCCCGAGTGCACAGCCCGCGGGGAACTTGTGTTGATGCAGTGTGACGCCCGCG	616
	541	CG 542	
	617	GG 618	
T 8			
521	CR619521	1049 bp mRNA linear HTC 21-JUL-2004	
ITION	Full-length cDNA clone CS0D1084YK05 of Placenta Cot 25-normalized		
SION	CR619521		
3DN	CR619521.1 GI:50500328		
ZDS	HTC; CNSTL cDNA.		
3	Homo sapiens (human)		
ANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homidae; Homo.		
ENCE	1 (bases 1 to 1049)		
HORS	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.		
LE	Full-length cDNA libraries and normalization		
RNAL	Unpublished		
ARK	Contact : Feng Liang Email : fliang@lifetech.com URL :		
	http://fulllength.invitrogen.com/Invitrogen Corporation 1600		
	Parday Avenue		
	2 (baes 1 to 1049)		
ENCE	Genoscope.		
HORS	Direct Submission		
LE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :		
RNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr		
	- Web : www.genoscope.cns.fr)		
NT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primes		
	end enriched, double-strand cDNA was digested with Not I and cloned		
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
	was normalized. Library was constructed by Life Technologies, a		
	division of Invitrogen.		
RES	Location/Qualifiers		
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ches 542; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
1 CTGGTTGATGCACTATGACTCTGGAAGAAGTCCGGCGCACGACACAGTTCCGGAAGC	60		

Db	79	CTGGTTGATGCGCACTAATGACCTCTGGAAAGAAAGTCGGCGGCGCAGGACACAGTTCTCGGAAAGC	138
Qy	61	ACAGCCAGGATGCAAGGGTCCGGGAAAGCCGTCGATGAGTTGCTGCTGTCCGCGCAGCGT	120
Db	139	ACAGCCAGGATGCAAGGGTCCGGGAAAGCCGTCGATGAGTTGCTGCTGTCCGCGCAGCGT	198
Qy	121	CAGGGCTGCCCTCACCTGCCGGGCGTACAGAGTCAGCCAAAGTCTTGAAAGCTGGAGCCCGGAC	180
Db	199	CAGGGCTGCCCTCACCTGCCGGGCGTACAGAGTCAGCCAAAGTCTTGAAAGCTGGAGCCCGGAC	258
Qy	181	AATGTGACCTTCTGTGTGCTGGCTGCGGGTGGAGAGACGAGGGCGGACATCGCGCTGCAG	240
Db	259	AATGTGACCTTCTGTGTGCTGGCTGCGGGTGGAGAGACGAGGGCGGACATCGCGCTGCAG	318
Qy	241	ATCCATTTTACGCTGATCCAGGCTTTCTGTGCTCGGAAACGACATGACATATGATGGCGGTG	300
Db	319	ATCCATTTTACGCTGATCCAGGCTTTCTGTGCTCGGAAACGACATGACATATGATGGCGGTG	378
Qy	301	GGCGATGTGACGCGGCTGGCGGGCTATCTGTGGCGCGCGCGCGAGAGAGCGGGGTGCGCGGCG	360
Db	379	GGCGATGTGACGCGGCTGGCGGGCTATCTGTGGCGCGCGCGCGAGAGAGCGGGGTGCGCGGCG	438
Qy	361	GACCTGCACCTGATCCTCATTTTCGAAACCCCAACGAGAGACGCTGTGAAGAGATCCCGGCTTG	420
Db	439	GACCTGCACCTGATCCTCATTTTCGAAACCCCAACGAGAGACGCTGTGAAGAGATCCCGGCTTG	498
Qy	421	GAGAACTCAGACTGTGTTTTTCGAGAGAGCCGCGACGTTTAAACGACTGGGTGCCAGCATC	480
Db	499	GAGAACTCAGACTGTGTTTTTCGAGAGAGCCGCGACGTTTAAACGACTGGGTGCCAGCATC	558
Qy	481	ACCCTGCCGAGTGCACACCCCGGCGGGACCTTGGTCTGATCGAGTGGTGAAGCCCGCGG	540
Db	559	ACCCTGCCGAGTGCACACCCCGGCGGGACCTTGGTCTGATCGAGTGGTGAAGCCCGCGG	618
Qy	541	GG 542	
Db	619	GG 620	

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 DEFINITION Full-length cDNA clone CSD01034719 of Placenta Cot 25-normalized  
 of Homo sapiens (human).  
 ACCESSION CR617419  
 VERSION CR617419.1 GI:50498226  
 KEYWORDS HTC; cNSLT cDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 1052)  
 Li, W.B., Gruber C., Jesse, J. and Polayes D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 Contact : Feng Liang Email : fliang@lifeitech.com URL :  
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
 Faraday Avenue  
 2 (bases 1 to 1052)  
 Genoscope.  
 Direct Submission  
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
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Match 98.4%; Score 542; DB 6; Length 1052;  
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Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGGTGTATGCACTATGACTCTGGAAGAGTCCGGCGCCAGACACAGTTCGGGAAGC 60  
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92 CTGGTGTATGCACTATGACTCTGGAAGAGTCCGGCGCCAGACACAGTTCGGGAAGC 151  
61 ACAGCCAGATGAGAGGTGCGGGAAAGCGCTGATGAGTGTGCTGCTGGCGCAGCGT 120  
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152 ACAGCCAGATGAGAGGTGCGGGAAAGCGCTGATGAGTGTGCTGCTGGCGCAGCGT 211  
121 CAGGGCTGCTCACTGCGCGCTCTACAGAGTCAAGCCAAAGTCTTGAACGTGAACCCCGAC 180  
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212 CAGGGCTGCTCACTGCGCGCTCTACAGAGTCAAGCCAAAGTCTTGAACGTGAACCCCGAC 271  
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332 ATTCATTTTACGCTGATCCAGGCTTTCTGCTGAGAGACAGCATCCAGATAGTGGCGGTG 391  
301 GGGGATGTGAGAGCGGCTGCGGCTATGCTGAGCGCCCGCGAGAGAGCGGCTGCGCGGCG 360  
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392 GGGGATGTGAGAGCGGCTGCGGCTATGCTGAGCGCCCGCGAGAGAGCGGCTGCGCGGCG 451  
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452 GACCTGCACTGCACTCTGATTTTGAACCCCAAGAGAGACCGCTGGAAGATCCCGCTTG 511  
421 GAGAAGCTCAGCGCTGTTTGGAGAGAGCGCGGCTTAAAGCATGGGTGCCAGATC 480  
|||||  
512 GAGAAGCTCAGCGCTGTTTGGAGAGAGCGCGGCTTAAAGCATGGGTGCCAGATC 571  
481 ACCCTCCCGAGTGAACAGCCCGCGGAGCTTGTGTGATCGACGTGTGACGCCCGCG 540  
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572 ACCCTCCCGAGTGAACAGCCCGCGGAGCTTGTGTGATCGACGTGTGACGCCCGCG 631  
541 GG 542  
||  
632 GG 633

T 10 1062 bp mRNA linear HTC 21-JUL-2004  
382 full-length cDNA clone CS01034YD21 of Placenta Cot 25-normalized  
ITITON of Homo sapiens (human).  
STION CR591382.1 GI:50472189  
ON CR591382.1 GI:50472189  
RDS Homo sapiens (human)  
E Homo sapiens  
ANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo  
1 (bases 1 to 1062)  
ENCE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
HORS Full-length cDNA libraries and normalization  
LE Unpublished  
RNAL Contact: Feng Liang Email: fliang@lifetech.com URL:  
ARK http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Parade Avenue  
2 (bases 1 to 1062)

AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr)  
COMMENT - Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
FEATURES  
source Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="CS01034YD21"  
/issue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

# ORIGIN

Query Match 98.4%; Score 542; DB 6; Length 1062;  
Best Local Similarity 100.0%; Pred. No. 7.8e-120;  
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGGTGTATGCACTATGACTCTGGAAGAGTCCGGCGCCAGACACAGTTCGGGAAGC 60  
|||||  
92 CTGGTGTATGCACTATGACTCTGGAAGAGTCCGGCGCCAGACACAGTTCGGGAAGC 151  
61 ACAGCCAGATGAGAGGTGCGGGAAAGCGCTGATGAGTGTGCTGCTGGCGCAGCGT 120  
|||||  
152 ACAGCCAGATGAGAGGTGCGGGAAAGCGCTGATGAGTGTGCTGCTGGCGCAGCGT 211  
121 CAGGGCTGCTCACTGCGCGCTCTACAGAGTCAAGCCAAAGTCTTGAACGTGAACCCCGAC 180  
|||||  
212 CAGGGCTGCTCACTGCGCGCTCTACAGAGTCAAGCCAAAGTCTTGAACGTGAACCCCGAC 271  
181 AATGTGACCTTCTGTGTGCTGCTGCGGTGAGAGAGACAGGCGCATGCGGCTGACAG 240  
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272 AATGTGACCTTCTGTGTGCTGCTGCGGTGAGAGAGACAGGCGCATGCGGCTGACAG 331  
241 ATTCATTTTACGCTGATCCAGGCTTTCTGCTGAGAGACAGCATCCAGATAGTGGCGGTG 300  
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332 ATTCATTTTACGCTGATCCAGGCTTTCTGCTGAGAGACAGCATCCAGATAGTGGCGGTG 391  
301 GGGGATGTGAGAGCGGCTGCGGCTATGCTGAGCGCCCGCGAGAGAGCGGCTGCGCGGCG 360  
|||||  
392 GGGGATGTGAGAGCGGCTGCGGCTATGCTGAGCGCCCGCGAGAGAGCGGCTGCGCGGCG 451  
361 GACCTGCACTGCACTCTGATTTTGAACCCCAAGAGAGACCGCTGGAAGATCCCGCTTG 420  
|||||  
452 GACCTGCACTGCACTCTGATTTTGAACCCCAAGAGAGACCGCTGGAAGATCCCGCTTG 511  
421 GAGAAGCTCAGCGCTGTTTGGAGAGAGCGCGGCTTAAAGCATGGGTGCCAGATC 480  
|||||  
512 GAGAAGCTCAGCGCTGTTTGGAGAGAGCGCGGCTTAAAGCATGGGTGCCAGATC 571  
481 ACCCTCCCGAGTGAACAGCCCGCGGAGCTTGTGTGATCGACGTGTGACGCCCGCG 540  
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572 ACCCTCCCGAGTGAACAGCCCGCGGAGCTTGTGTGATCGACGTGTGACGCCCGCG 631  
541 GG 542  
||  
632 GG 633

RESULT 11  
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LOCUS 601296929F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822765 5',  
DEFINITION mRNA sequence.  
ACCESSION BF219948  
VERSION BF219948.1 GI:11126042  
KEYWORDS EST.

E Homo sapiens (human)  
 ANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 ENCE 1 (bases 1 to 718)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 HORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 LE Unpublished (1999)  
 RNAL Contact: Robert Strausberg, Ph. D.  
 NT Email: cgsabers@mail.nih.gov  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: IRAL1 row: j column: 07  
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 Location/Qualifiers  
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 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 7"  
 /note="Organ: lung; Vector: pOT87; Site 1: XhoI; Site 2:  
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 adaptor: GGACGAG(G). Size selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 N  
 Match 97.4%; Score 536.8; DB 7; Length 718;  
 Local Similarity 99.5%; Pred. No. 1,4e-118;  
 ches 549; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
 1 CTGGTTGATGCACTATGACTCTTGGAAGAGTCCGCGCCAGACACAGTCCGGAAGC 60  
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 61 ACAGCCAGATGAGAGGTCGCGGAAAGCCCTGATAGTTGCTGTGCGCGACGCT 120  
 118 ACAGCCAGATGAGAGGTCGCGGAAAGCCCTGATAGTTGCTGTGCGCGACGCT 177  
 121 CAGGGCTGCTCACTGCGGCGCTTACGAGTCAAGCCAAATCTTGAACGTGACCCGAC 180  
 178 CAGGGCTGCTCACTGCGGCGCTTACGAGTCAAGCCAAATCTTGAACGTGACCCGAC 237  
 181 AATGTGACCTTCTGTGTGCTGCGGTGAGAGAGACGAGCCGATCCGCGTCCAG 240  
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 241 ATCATTTTACGCTGATCCAGGCTTTCTGTGCTGAGAGACATCGACATAGTCCGCTG 300  
 298 ATCATTTTACGCTGATCCAGGCTTTCTGTGCTGAGAGACATCGACATAGTCCGCTG 357  
 301 GGGGATGTGACGCGGCTGCGGCTATGATGAGGCGCGGAGAGAGGCGGCTGCGCGGC 360  
 358 GGGGATGTGACGCGGCTGCGGCTATGATGAGGCGCGGAGAGAGGCGGCTGCGCGGC 417  
 361 GACCTGACATGACATCCATTTTGAACCCAGAGAGACGCTGAGAGATCCCGGCTG 420  
 418 GACCTGACATGACATCCATTTTGAACCCAGAGAGACGCTGAGAGATCCCGGCTG 477  
 421 GAGAAGCTCAAGCTGTTTTCGAGAGAGAGCGCAGCTTAAAGATGGGTGCCAGATC 480  
 478 GAGAAGCTCAAGCTGTTTTCGAGAGAGAGCGCAGCTTAAAGATGGGTGCCAGATC 537

QY 481 ACCCTCCCCGAGTGAACAGCCCGCGGAGACCTTGTGTC-TGATCGACGTGTGACGCCCGC 539  
 Db 538 ACCCTCCCCGAGTGAACAGCCCGCGGAGACCTTGTGTCGTGATGACGTGTGACGCCCGC 597  
 QY 540 GGGGCTGAGAC 551  
 Db 598 GGGGCTGAGAC 609  
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 DEFINITION clone CS0D1029Y017 3-PRIME, mRNA sequence.  
 ACCESSION BX379029  
 VERSION BX379029.2 GI:46575194  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 1011)  
 AUTHORS Li W.B., Gruber C., Jessee J. and Polayes D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On May 8, 2003 this sequence version replaced gi:30450722.  
 CONTACT: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 5465.f  
 For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?c=CS0D1029AH09NP1c=5465.f>.  
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."  
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 Query Match 96.4%; Score 531.4; DB 4; Length 1011;  
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 1 CTGGTTGATGCACTATGACTCTTGGAAGAGTCCGCGCCAGACACAGTCCGGAAGC 60  
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 61 ACAGCCAGATGAGAGGTCGCGGAAAGCCCTGATAGTTGCTGTGCGCGACGCT 120  
 876 ACAGCCAGATGAGAGGTCGCGGAAAGCCCTGATAGTTGCTGTGCGCGACGCT 817  
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 816 CAGGGCTGCTCACTGCGGCGCTTACGAGTCAAGCCAAATCTTGAACGTGACCCGAC 757  
 181 AATGTGACCTTCTGTGTGCTGCGGTGAGAGAGACGAGGCGACATCGCGTCCAG 240  
 756 AATGTGACCTTCTGTGTGCTGCGGTGAGAGAGACGAGGCGACATCGCGTCCAG 697

241 ATCCATTTTACGCTGATCCAGGCTTCTGCTGAGAGACGATCCGATAGTGCAGG 300  
 696 ATCCATTTTACGCTGATCCAGGCTTCTGCTGAGAGACGATCCGATAGTGCAGG 637  
 301 GGGGATGTGACGCGCTGCGGCTATGCTGGCGCGCGGAGAGCGGGTGGCGGGC 360  
 636 GGGGATGTGACGCGCTGCGGCTATGCTGGCGCGCGGAGAGCGGGTGGCGGGC 577  
 361 GACCTGACCTGCATCTTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCCGCTTG 420  
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 516 GAGAGCTGACCTGTTTTCGAGAGAGCGGAGCTTAAGACTGGTGGCCAGATC 457  
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 541 GG 542  
 396 GG 395

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 ON B1117459  
 RDS B1117459.1 GI:14568360  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

ENCE 1 (bases 1 to 774)  
 HORS NIH-MGC http://mgi.nci.nih.gov/  
 LE National Institutes of Health, Mammalian Gene Collection (MGC)  
 RNAL Unpublished (1999)  
 NT Contact: Robert Strausberg, Ph.D.  
 Email: rgs@bbs-rmail.nih.gov  
 Tissue Procurement: DCM/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LIML at: image.llnl.gov  
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RES Location/Qualifiers

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 /clone="IMAGE:5016316"  
 /tissue\_type="small cell carcinoma"  
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 /lab\_host="NIH MGC 7"  
 /note="Organ: lung; Vector: pORF7; Site 1: XhoI; Site 2:  
 EcoRI; CDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-CDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 96.4%; Score 531; DB 2; Length 774;  
 Best Local Similarity 99.8%; Pred. No. 3.4e-117;  
 Matches 542; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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 196 CAGGCTGCTTCACTCCGCGGCTCTAGAGTCCGCGGCGAGACACAGTTCCGAAAGC 255  
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 496 GAGAGCTGACCTGTTTTCGAGAGAGCGGAGCTTAAGACTGGTGGCCAGATC 555  
 481 ACCCTCCCGAGTGACAGCCCGGCGGAGCTTGTCTGATCCAGCTGTGACGCCCGG 539  
 556 ACCCTCCCGAGTGACAGCCCGGCGGAGCTTGTCTGATCCAGCTGTGACGCCCGG 615  
 540 GGG 542  
 616 GGG 618

## RESULT 14

BX397383

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX397383 1041 bp mRNA linear EST 28-APR-2004  
 BX397383 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA  
 clone CSOD1034YD21 5-PRIME, mRNA sequence.  
 BX397383  
 BX397383.2 GI:146835270  
 EST.  
 Homo sapiens (human)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 1041)  
 Li, W.B., Gruber, C.J., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On May 13, 2003 this sequence version replaced gi:30609433.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE  
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr  
 1st strand cDNA was primed with a NciI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Nci I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 5465.f

For more information about this cluster, see  
<http://www.genoscope.cns.fr/cda?c=CSODI034CB110P1&c=5465.f>.

RES Location/Qualifiers  
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N  
 ry Match 96.1%; Score 529.6; DB 4; Length 1041;  
 Local Similarity 99.6%; Pred. No. 7.6e-117; Indels 1; Gaps 1;  
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 mRNA sequence.  
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 DN B1917007.1 GI:16180958  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

# REFERENCE

1 (bases 1 to 594)  
 NIH-MGC <http://mhc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 Tissue Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
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# FEATURES

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# ORIGIN

Query Match 96.1%; Score 529.4; DB 2; Length 594;  
 Best Local Similarity 99.6%; Pred. No. 8.1e-117;  
 Matches 541; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Rank	Score	Query Match	Length	ID	Description
1	542	98.4	1065	2 US-08-463-081B-11	Sequence 11, Appl
2	542	98.4	1065	2 US-08-461-379A-11	Sequence 11, Appl
3	542	98.4	1065	2 US-08-462-390B-11	Sequence 11, Appl
4	542	98.4	1065	3 US-08-463-074B-11	Sequence 11, Appl
5	542	98.4	1065	3 US-08-465-585C-11	Sequence 11, Appl
6	542	98.4	1065	3 US-08-652-446-11	Sequence 11, Appl
7	542	98.4	1065	3 US-09-949-016-3873	Sequence 3873, Ap
8	542	98.4	1065	3 US-09-879-833-1	Sequence 1, Appl
9	538.8	97.8	1036	2 US-08-797-831A-3	Sequence 3, Appl
10	527.8	95.8	750	2 US-09-023-655-820	Sequence 820, Ap
11	477	86.6	477	2 US-08-463-081B-31	Sequence 31, Appl
12	477	86.6	477	2 US-08-461-379A-31	Sequence 31, Appl
13	477	86.6	477	2 US-08-462-390B-31	Sequence 31, Appl
14	477	86.6	477	3 US-08-463-074B-31	Sequence 31, Appl
15	477	86.6	477	3 US-08-465-585C-31	Sequence 31, Appl
16	477	86.6	477	3 US-08-652-446-31	Sequence 31, Appl
17	473.8	86.0	477	2 US-08-797-831A-2	Sequence 2, Appl
18	274	49.7	4444	3 US-09-879-833-3	Sequence 3, Appl
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21	172.4	31.3	745	2 US-08-602-208-1	Sequence 1, Appl
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25	154.4	28.0	1343	4 US-09-880-107-2268	Sequence 2368, Ap
26	154.4	28.0	1343	5 US-10-600-158-1	Sequence 1, Appl
27	154.4	28.0	1366	3 US-09-919-172-59	Sequence 59, Appl
28	143.6	26.1	204	2 US-08-330-108-11	Sequence 11, Appl
29	143.6	26.1	204	7 PCT-US92-10087-11	Sequence 11, Appl
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31	93.8	17.0	5999	3 US-09-949-016-13536	Sequence 13536, A
32	86	15.6	431	4 US-09-880-107-1152	Sequence 1152, Ap
33	84.2	15.3	227	7 PCT-US92-10087-13	Sequence 13, Appl
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35	69	12.5	601	3 US-09-949-016-137771	Sequence 137771, A
36	59.2	10.7	150	2 US-08-330-108-14	Sequence 14, Appl
37	59.2	10.7	150	7 PCT-US92-10087-14	Sequence 14, Appl
38	59.2	10.7	403	3 US-09-513-999C-2210	Sequence 2210, Ap
39	56.8	10.3	53799	3 US-10-042-665A-3	Sequence 3, Appl
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42	49.8	9.0	1581	3 US-09-902-540-9170	Sequence 9170, Ap
43	49.8	9.0	1612	3 US-09-902-540-981	Sequence 981, Ap
44	47.2	8.6	17938	3 US-09-902-540-1111	Sequence 1111, Ap
45	45.8	8.3	684	3 US-09-252-991A-11767	Sequence 11767, A

## ALIGNMENTS

RESULT 1  
US-08-463-081B-11  
Sequence 11, Application US/08463081B  
Patent No. 5871960  
Patent No. 5871960 5837487  
GENERAL INFORMATION:  
APPLICANT: Smith, Kendall A. & Beadling, Carol  
TITLE OF INVENTION: Nucleic Acids Encoding CRS Polypeptide,  
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
STREET: 444 South Flower St. - Suite 1900  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,081B  
FILING DATE: 5-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/104,736  
FILING DATE: 10-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,066  
FILING DATE: 20-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Viviana Amzel, Ph. D.  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 622-7700  
TELEFAX: (213) 489-4210  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1065 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA



quence 11, Application US/08462390B  
 Patent No. 5882894

GENERAL INFORMATION:  
 APPLICANT: Smith, K. A., & Beadling, C.  
 TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and  
 TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ratner & Prestia  
 ADDRESS: (B) STREET: One Westlakes-Berwyn  
 CITY: Valley Forge  
 STATE: Pennsylvania  
 COUNTRY: USA  
 ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/462,390B  
 FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/330,108  
 FILING DATE: 27-OCT-1994  
 APPLICATION NUMBER: USSN 08/104,736  
 FILING DATE: 10-AUG-1993  
 APPLICATION NUMBER: USSN 07/796,066  
 FILING DATE: 20-NOV-91

ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: DART-040  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610)407-0700  
 TELEFAX: (610)407-0701

INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1065 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 98..575  
 B-462-390B-11

Query Match 98.4%; Score 542; DB 2; Length 1065;  
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Db 623 GG 624
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RESULT 4

US-08-463-074B-11  
 Sequence 11, Application US/08463074B  
 Patent No. 6020155  
 GENERAL INFORMATION:  
 APPLICANT: Smith, Kendall A., & Beadling, Carol  
 TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PRETTY, SCROEDER & POPLAWSKI  
 ADDRESS: (B) STREET:  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0,  
 SOFTWARE: Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/463,074B  
 FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/104,736  
 FILING DATE: 10-AUG-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796,066  
 FILING DATE: 20-NOV-91

ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 622-7700

INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1065 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 98..575  
 US-08-463-074B-11

Query Match 98.4%; Score 542; DB 3; Length 1065;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;  
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGTTGATCGACTATGACTCTTGAGAAAGTCCCGCGCCAGACACAGTTCCGAAAC 60  
 83 CTGTTGATCGACTATGACTCTTGAGAAAGTCCCGCGCCAGACACAGTTCCGAAAC 142  
 61 ACAGCCAGATGACAGGATGACCGGAAAGGCTGACATGATGCTGTGTCGCGGACGCT 120  
 143 ACAGCCAGATGACAGGATGACCGGAAAGGCTGACATGATGCTGTGTCGCGGACGCT 202  
 121 CAGGCTGCTCACTGCTCCGCGCTCTACAGTACAGTACAGTACAGTACAGTACAGT 180  
 203 CAGGCTGCTCACTGCTCCGCGCTCTACAGTACAGTACAGTACAGTACAGTACAGT 262  
 181 AATGTACCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 263 AATGTACCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 322  
 241 ATCCATTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
 323 ATCCATTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 382  
 301 GGCAGATGTCAGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 383 GGCAGATGTCAGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 442  
 361 GACCTGCACTGATCTCTCATTTTGAAACCCCAAGAGAGAGAGAGAGAGAGAGAGAG 420  
 443 GACCTGCACTGATCTCTCATTTTGAAACCCCAAGAGAGAGAGAGAGAGAGAGAGAG 502  
 421 GAGAGCTCAGAGCTGTTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
 503 GAGAGCTCAGAGCTGTTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 562  
 481 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTGATGATGATGATGATGATGATGATG 540  
 563 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTGATGATGATGATGATGATGATGATG 622  
 541 GG 542  
 623 GG 624

T 5  
 1-465-585C-11  
 uence 11, Application US/08465585C  
 ent No. 6027914  
 NERAL INFORMATION:  
 APPLICANT: Smith, K. A., & Beadling, C.  
 TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector  
 TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 900071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Releasee #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/465,585C  
 FILING DATE: 5-JUNE-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/330,108  
 FILING DATE: 27-OCT-1994  
 APPLICATION NUMBER: USSN 08/104,736  
 FILING DATE: 10-AUG-1993  
 APPLICATION NUMBER: USSN 07/796,066  
 FILING DATE: 20-NOV-1991  
 ATTORNEY/AGENT INFORMATION:

444South Flower St. - Suite 190

NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 622-7700  
 TELEFAX: (213) 4894210  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1065 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 98..575  
 US-08-465-585C-11

Query Match 98.4%; Score 542; DB 3; Length 1065;  
 Best Local Similarity 100.0%; Fred. No. 1.9e-115;  
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGTTGATCGACTATGACTCTTGAGAAAGTCCCGCGCCAGACACAGTTCCGAAAC 60  
 DB 83 CTGTTGATCGACTATGACTCTTGAGAAAGTCCCGCGCCAGACACAGTTCCGAAAC 142  
 QY 61 ACAGCCAGATGACAGGATGACCGGAAAGGCTGACATGATGCTGTGTCGCGGACGCT 120  
 DB 143 ACAGCCAGATGACAGGATGACCGGAAAGGCTGACATGATGCTGTGTCGCGGACGCT 202  
 QY 121 CAGGCTGCTCACTGCTCCGCGCTCTACAGTACAGTACAGTACAGTACAGTACAGT 180  
 DB 203 CAGGCTGCTCACTGCTCCGCGCTCTACAGTACAGTACAGTACAGTACAGTACAGT 262  
 QY 181 AATGTACCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 DB 263 AATGTACCTTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 322  
 QY 241 ATCCATTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300  
 DB 323 ATCCATTTTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 382  
 QY 301 GGCAGATGTCAGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 DB 383 GGCAGATGTCAGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 442  
 QY 361 GACCTGCACTGATCTCTCATTTTGAAACCCCAAGAGAGAGAGAGAGAGAGAGAGAG 420  
 DB 443 GACCTGCACTGATCTCTCATTTTGAAACCCCAAGAGAGAGAGAGAGAGAGAGAGAG 502  
 QY 421 GAGAGCTCAGAGCTGTTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
 DB 503 GAGAGCTCAGAGCTGTTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 562  
 QY 481 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTGATGATGATGATGATGATGATGATG 540  
 DB 563 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTGATGATGATGATGATGATGATGATG 622  
 QY 541 GG 542  
 DB 623 GG 624

RESULT 6  
 US-08-652-446-11  
 ; Sequence 11, Application US/08652446  
 ; Patent No. 6057427  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smith, Kendall A. & Beadling, Carol  
 ; TITLE OF INVENTION: Nucleic Acids Encoding CR5  
 ; TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and  
 ; NUMBER OF SEQUENCES: 38

## CORRESPONDENCE ADDRESS:

ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
 ADDRESS: (B) STREET:  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA

444 South Flower St. - Suite 1900

ZIP: 90071

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0,  
 SOFTWARE: Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/652,446

## FILING DATE:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP App. # 96921319.8  
 FILING DATE: 5-JAN-1998

APPLICATION NUMBER: PCT/US/96/09194  
 FILING DATE: 5-JUN-1996

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/330,108  
 FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/463,074  
 FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/462,337  
 FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/462,390  
 FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/465,585  
 FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/463,081  
 FILING DATE: 5-JUN-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/461,379  
 FILING DATE: 5-JUN-1991

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/739,523  
 FILING DATE: 29-OCT-1996

ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: PP66 40035  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 622-7700

TELEFAX: (213) 489-4210  
 INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 1065 base pairs  
 TYPE: nucleic acid

STRANDEDNESS: single  
 TOPOLOGY: linear

MOLECULE TYPE: cDNA  
 FEATURE:

NAME/KEY: CDS  
 LOCATION: 98..575

8-652-446-11

98.4% Score 542; DB 3; Length 1065;

100.0% Pred. No. 1.9e-115; Indels 0; Gaps 0;

542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGGTTGATGCACTATGACTCTGGAAGAGTCCGCGCCAGGACACAGTTCCGGAAGC 60

83 CTGGTTGATGCACTATGACTCTGGAAGAGTCCGCGCCAGGACACAGTTCCGGAAGC 142

61 ACAGCCAGATGACAGGGTCCGCGGAAGCCGCTGCATGAGTTGCTGCGCGCAGCGT 120

143 ACAGCCAGATGACAGGGTCCGCGGAAGCCGCTGCATGAGTTGCTGCGCGCAGCGT 202

121 CAGGGCTGCTCACTGCGCGCGCTTACGAGTCAAGCCAAAGTTTGAAGCTGACCCGAC 180

203 CAGGGCTGCTCACTGCGCGCGCTTACGAGTCAAGCCAAAGTTTGAAGCTGACCCGAC 262

181 AATGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

263 AATGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 322

241 ATCCATTTTACGCTGATCCAGGCTTCTGCTGAGAGACAGATCAGATAGTCCGCTG 300

323 ATCCATTTTACGCTGATCCAGGCTTCTGCTGAGAGACAGATCAGATAGTCCGCTG 382

301 GCGATGTCAGCGGCTGCGCGCTTACGAGTCAAGCCAAAGTTTGAAGCTGACCCGAC 360

383 GCGATGTCAGCGGCTGCGCGCTTACGAGTCAAGCCAAAGTTTGAAGCTGACCCGAC 442

361 GACCTGCACTGATCTCTCATTTTGAACCCCAACGAGAGAGCCCTGGAAGATCCCGCTTG 420

443 GACCTGCACTGATCTCTCATTTTGAACCCCAACGAGAGAGCCCTGGAAGATCCCGCTTG 502

421 GAGAGCTGAGCTGTTTTCGAGAGAGCCGAGGCTTAAAGATGAGTCCAGCATC 480

503 GAGAGCTGAGCTGTTTTCGAGAGAGCCGAGGCTTAAAGATGAGTCCAGCATC 562

481 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTCTGATGACGCTGAGCCGCCG 540

563 ACCCTCCCGAGTACAGCCCGCGGAGACCTTGTCTGATGACGCTGAGCCGCCG 622

541 GG 542

623 GG 624

RESULT 7

US-09-949-016-3873

Sequence 3873, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTNER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3873

LENGTH: 1065

TYPE: DNA

ORGANISM: Human

US-09-949-016-3873

Query Match

98.4% Score 542; DB 3; Length 1065;

100.0% Pred. No. 1.9e-115; Indels 0; Gaps 0;

542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGGTTGATGCACTATGACTCTGGAAGAGTCCGCGCCAGGACACAGTTCCGGAAGC 60

95 CTGGTTGATGCACTATGACTCTGGAAGAGTCCGCGCCAGGACACAGTTCCGGAAGC 154

61 ACAGCCAGATGACAGGGTCCGCGGAAGCCGCTGCATGAGTTGCTGCGCGCAGCGT 120

155 ACAGCCAGATGACAGGGTCCGCGGAAGCCGCTGCATGAGTTGCTGCGCGCAGCGT 214





LOCATION: 84..560  
8-797-831A-3

Query Match 97.8%; Score 538.8; DB 2; Length 1036;  
% Local Similarity 99.4%; Pred. No. 1.1e-114;  
Matches 540; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1 CTGGTGTGATGCGACTATGACTGTGAGAAAGTCCGGCGGCGAGGACACAGTTCCGGAAGC 60
  CTGGTGTGATGCGACTATGACTGTGAGAAAGTCCGGCGGCGAGGACACAGTTCCGGAAGC 128
69 CTGGTGTGATGCGACTATGACTGTGAGAAAGTCCGGCGGCGAGGACACAGTTCCGGAAGC 128
129 ACAGCCAGGATGCGAGGATGCGGGAAGCCCTCATAGTGTGCTGTGCGGCGACGCT 188
61 ACAGCCAGGATGCGAGGATGCGGGAAGCCCTCATAGTGTGCTGTGCGGCGACGCT 120
121 CAGGGCTGCTCACTGCGGCGCTCTACGATTCAGCCAAATCTTGAACGTTGACCCCGAC 180
189 CAGGGCTGCTCACTGCGGCGCTCTACGATTCAGCCAAATCTTGAACGTTGACCCCGAC 248
181 AATGTGACCTTCTGTGTGCTGTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
249 AATGTGACCTTCTGTGTGCTGTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 308
241 ATCCATTTTACGCTGATTCAGGCTTTCTGCTGCGAGAACATCGACATAGTGCCTGTG 300
309 ATCCATTTTACGCTGATTCAGGCTTTCTGCTGCGAGAACATCGACATAGTGCCTGTG 368
301 GGGGATGTGACGGGCTGTGGGCTATGCTGAGGCGCGGCGAGGAGGCGGGTGGCGGGC 360
369 GGGGATGTGACGGGCTGTGGGCTATGCTGAGGCGCGGCGAGGAGGCGGGTGGCGGGC 428
361 GACCTGACGTGCAATCTCATTTTGCAGACCCCAACGAGAGCCCTGGAAGATCCCGCCTTG 420
429 GACCTGACGTGCAATCTCATTTTGCAGACCCCAACGAGAGCCCTGGAAGATCCCGCCTTG 488
421 GAGAACTGACGCTGTTTGTGAGAGAGCGCGACGCTTAAACGATGGGTGCCAGCATC 480
489 GAGAACTGACGCTGTTTGTGAGAGAGCGCGACGCTTAAACGATGGGTGCCAGCATC 548
481 ACCCTCCCGAGTGAACAGCCCGGCGGAGCCTTGTGTCGATTCGAGCGTGAAGCGCCCGG 540
549 ACCCTCCCGAGTGAACAGCCCGGCGGAGCCTTGTGTCGATTCGAGCGTGAAGCGCCCGG 608
541 GG 542
609 GG 610

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1/7 10  
9-023-655-820  
Sequence 820 Application US/09023655  
Patent No. 6607879  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023.655

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? FILING DATE: HEREWITH
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER:
? FILING DATE:
? CLASSIFICATION:
? ATTORNEY/AGENT INFORMATION:
? NAME: Zeller, Karen J.
? REGISTRATION NUMBER: 37,071
? REFERENCE/DOCKET NUMBER: PA-0001 US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (650) 855-0555
? TELEFAX: (650) 845-4166
? INFORMATION FOR SEQ ID NO: 820:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 750 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? IMMEDIATE SOURCE:
? LIBRARY: PROSTUT04
? CLONE: 828764
? US-09-023-655-820

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Query Match 95.8%; Score 527.8; DB 3; Length 750;  
Best Local Similarity 99.4%; Pred. No. 3.4e-112;  
Matches 540; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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1 CTGGTGTGATGCGACTATGACTGTGAGAAAGTCCGGCGGCGAGGACACAGTTCCGGAAGC 60
84 CTGGTGTGATGCGACTATGACTGTGAGAAAGTCCGGCGGCGAGGACACAGTTCCGGAAGC 143
61 ACAGCCAGGATGCGAGGATGCGGGAAGCCCTCATAGTGTGCTGTGCGGCGACGCT 120
144 ACAGCCAGGATGCGAGGATGCGGGAAGCCCTCATAGTGTGCTGTGCGGCGACGCT 203
121 CAGGGCTGCTCACTGCGGCGCTCTACGATTCAGCCAAATCTTGAACGTTGACCCCGAC 180
204 CAGGGCTGCTCACTGCGGCGCTCTACGATTCAGCCAAATCTTGAACGTTGACCCCGAC 263
181 AATGTGACCTTCTGTGTGCTGTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240
264 AATGTGACCTTCTGTGTGCTGTGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 323
241 ATCCATTTTACGCTGATTCAGGCTTTCTGCTGCGAGAACATCGACATAGTGCCTGTG 300
324 ATCCATTTTACGCTGATTCAGGCTTTCTGCTGCGAGAACATCGACATAGTGCCTGTG 383
301 GGGGATGTGACGGGCTGTGGGCTATGCTGAGGCGCGGCGAGGAGGCGGGTGGCGGGC 360
384 GGGGATGTGACGGGCTGTGGGCTATGCTGAGGCGCGGCGAGGAGGCGGGTGGCGGGC 443
361 GACCTGACGTGCAATCTCATTTTGCAGACCCCAACGAGAGCCCTGGAAGATCCCGCCTT 419
444 GACCTGACGTGCAATCTCATTTTGCAGACCCCAACGAGAGCCCTGGAAGATCCCGCCTT 503
420 GAGAACTGACGCTGTTTGTGAGAGAGCCCGGAGCCTTGAACGATGGGTGCCAGCAT 479
504 GAGAACTGACGCTGTTTGTGAGAGAGCCCGGAGCCTTGAACGATGGGTGCCAGCAT 563
480 CACCTCCCGAGTGAACAGCCCGGCGGAGCCTTGTGTCGATTCGAGCGTGAAGCGCCCG 539
564 CACCTCCCGAGTGAACAGCCCGGCGGAGCCTTGTGTCGATTCGAGCGTGAAGCGCCCG 623
540 GGG 542
624 GGG 626

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RESULT 11  
US-08-463-081B-31  
Sequence 31, Application US/08463081B  
Patent No. 5871960

ent No. 5871960 5837487  
 GENERAL INFORMATION:  
 APPLICANT: Smith, Kendall A. & Beadling, Carol  
 TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,  
 TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
 STREET: 444 South Flower St. - Suite 1900  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0,  
 SOFTWARE: Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/463,081B  
 FILING DATE: 5-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/104,736  
 FILING DATE: 10-AUG-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796,066  
 FILING DATE: 20-NOV-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 622-7700  
 TELEFAX: (213) 489-4210  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 477 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 1-463-081B-31

Query Match 86.6%; Score 477; DB 2; Length 477;  
 Local Similarity 100.0%; Pred. No. 1.5e-100; Indels 0; Gaps 0;  
 ches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 16 ATGACTCTGGAAGAAGTCCGCGGCGCAGACAGATTCCGGAAGACACAGCCAGATGACG 75  
 1 ATGACTCTGGAAGAAGTCCGCGGCGCAGACAGATTCCGGAAGACACAGCCAGATGACG 60  
 76 GGTGCGGGGAAAGCGCTGCATGATGTTGCTGCTGCGCGCAGCGTCAAGGCTGCTCACT 135  
 61 GGTGCGGGGAAAGCGCTGCATGATGTTGCTGCTGCGCGCAGCGTCAAGGCTGCTCACT 120  
 136 GCGGCGGTCTACGAGTCAAGCCAAAGTCTTAAGCTGAGACCCCGACCAATGACCTTCTGT 195  
 121 GCGGCGGTCTACGAGTCAAGCCAAAGTCTTAAGCTGAGACCCCGACCAATGACCTTCTGT 180  
 196 GTGCTGGCTGCGGGGTGAGAGAGCAGAGGGAGCATGCGCTGCAGATTCATTTTAAGCTG 255  
 181 GTGCTGGCTGCGGGGTGAGAGAGCAGAGGGAGCATGCGCTGCAGATTCATTTTAAGCTG 240  
 256 ATCCAGGCTTTCTGCTGCGAAGACGATCAGATAGTGGCGGTGGCGATGTCAGCGG 315  
 241 ATCCAGGCTTTCTGCTGCGAAGACGATCAGATAGTGGCGGTGGCGATGTCAGCGG 300  
 316 CTGGCGGCTATCTGCGGCGCGCGGCGAGAGCGGGGTGCGCGGCGATCTGCACTGATC 375  
 301 CTGGCGGCTATCTGCGGCGCGCGGCGAGAGCGGGGTGCGCGGCGATCTGCACTGATC 360  
 376 CTGATTTTGAACCCCAAGAGAGCGCTGGAAGATCCGCTTGGGAAGTCAAGCTGAGCTG 435

Db 361 CTCATTTTGAACCCCAAGAGAGCGCTGGAAGATCCGCTTGGAGAGTCAAGCTG 420  
 Qy 436 TTTTGGAGAGAGCGCGCAGCTTAACGACTGGGTGCCAGCATCACTCCCGGAG 492  
 Db 421 TTTTGGAGAGAGCGCGCAGCTTAACGACTGGGTGCCAGCATCACTCCCGGAG 477

RESULT 12

US-08-461-379A-31  
 Sequence 31, Application US/08461379A  
 Patent No. 5871961

GENERAL INFORMATION:

APPLICANT: Smith, Kendall A. & Beadling, Carol  
 TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,  
 TITLE OF INVENTION: Vector and Transformed Cell Thereof, and  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ratner & Prestia  
 STREET: One Westlakes-Berwyn  
 CITY: Valley Forge  
 STATE: Pennsylvania  
 COUNTRY: USA  
 ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0,  
 SOFTWARE: Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/461,379A  
 FILING DATE: 5-JUNE-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/330,108; 08/104,736  
 APPLICATION NUMBER: & 07/796,066  
 FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: DART-070  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610)470-0700  
 TELEFAX: (610)470-0701  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 477 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-461-379A-31

Query Match 86.6%; Score 477; DB 2; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-100; Indels 0; Gaps 0;  
 Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGACTCTGGAAGAAGTCCGCGGCGCAGACAGATTCCGGAAGACACAGCCAGATGACG 75  
 Db 1 ATGACTCTGGAAGAAGTCCGCGGCGCAGACAGATTCCGGAAGACACAGCCAGATGACG 60  
 Qy 76 GGTGCGGGGAAAGCGCTGCATGATGTTGCTGCTGCGCGCAGCGTCAAGGCTGCTCACT 135  
 Db 61 GGTGCGGGGAAAGCGCTGCATGATGTTGCTGCTGCGCGCAGCGTCAAGGCTGCTCACT 120  
 Qy 136 GCGGCGGTCTACGAGTCAAGCCAAAGTCTTAAGCTGAGACCCCGACCAATGACCTTCTGT 195  
 Db 121 GCGGCGGTCTACGAGTCAAGCCAAAGTCTTAAGCTGAGACCCCGACCAATGACCTTCTGT 180  
 Qy 196 GTGCTGGCTGCGGGGTGAGAGAGCAGAGGGAGCATGCGCTGCAGATTCATTTTAAGCTG 255  
 Db 181 GTGCTGGCTGCGGGGTGAGAGAGCAGAGGGAGCATGCGCTGCAGATTCATTTTAAGCTG 240

256 ATCCAGGCTTTCTGCTGCGAGAGACATGATGCGCGCGCGCATGTGCGAGCG 315  
 241 ATCCAGGCTTTCTGCTGCGAGAGACATGATGCGCGCGCATGTGCGAGCG 300  
 316 CTGGCGGCTATCGTGGCGCGCGCGAGAGCGCGGTGCGCGCGCATGTGCGATC 375  
 301 CTGGCGGCTATCGTGGCGCGCGCGAGAGCGCGGTGCGCGCGCATGTGCGATC 360  
 376 CTGATTTGGAACCCCAACGAGAGCGCGTGAAGGATCCGCGCTTGGAGAACTCAGCGTG 435  
 361 CTGATTTGGAACCCCAACGAGAGCGCGTGAAGGATCCGCGCTTGGAGAACTCAGCGTG 420  
 436 TTTTGGAGAGAGCGCGCAGCGCTTAAAGACTGGGTGCCAGCATCACTCCCGAG 492  
 421 TTTTGGAGAGAGCGCGCAGCGCTTAAAGACTGGGTGCCAGCATCACTCCCGAG 477

1/1 13  
 11-462-390B-31  
 Invention 31, Application US/08462390B  
 Patent No. 5882894  
 GENERAL INFORMATION:  
 APPLICANT: Smith, K. A., & Beadling, C.  
 TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and  
 TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ratner & Prestia  
 ADDRESS: (B) STREET:One Westlakes-Berwyn  
 CITY: Valley Forge  
 STATE: Pennsylvania  
 COUNTRY: USA  
 ZIP: 19462

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/462,390B  
 FILING DATE: 5-JUNE-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/330,108  
 FILING DATE: 27-OCT-1994  
 APPLICATION NUMBER: USSN 08/104,736  
 FILING DATE: 10-AUG-1993  
 APPLICATION NUMBER: USSN 07/796,066  
 FILING DATE: 20-NOV-91  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: DART-040  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (610) 407-0700  
 TELEFAX: (610) 407-0701  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 477 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 B-462-390B-31

ery Match 86.6%; Score 477; DB 2; Length 477;  
 st Local Similarity 100.0%; Pred. No. 1.5e-100;  
 lches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

16 ATGACTCTGGAAGAGTCCGCGCCAGAGACAGTTCGGAAGAGAGCCAGGATGAG 75  
 1 ATGACTCTGGAAGAGTCCGCGCCAGAGACAGTTCGGAAGAGAGCCAGGATGAG 60

QY 76 GGTCCGCGAAGACCGCTGATGATGTTCTGTCTGCGCGCAGCGTCCGCTCACT 135  
 DB 61 GGTCCGCGAAGACCGCTGATGATGTTCTGTCTGCGCGCAGCGTCCGCTCACT 120  
 QY 136 GCGCGGCTTACGAGAGTCAAGCAAGCTTGAAGCTGAGCCCGACAACTGACTTCTGT 195  
 DB 121 GCGCGGCTTACGAGAGTCAAGCAAGCTTGAAGCTGAGCCCGACAACTGACTTCTGT 180  
 QY 196 GTGCTGCTGCGCGGTGAGAGAGAGAGCGCGCATGATGCGCGGTGAGAGAGTGAAGCTG 255  
 DB 181 GTGCTGCTGCGCGGTGAGAGAGAGAGCGCGCATGATGCGCGGTGAGAGAGTGAAGCTG 240  
 QY 256 ATCCAGGCTTTCTGCTGCGAGAGACGATGATGCGCGGTGAGAGAGTGAAGCTGACTG 315  
 DB 241 ATCCAGGCTTTCTGCTGCGAGAGACGATGATGCGCGGTGAGAGAGTGAAGCTGACTG 300  
 QY 316 CTGGCGGCTATCGTGGCGCGCGCGAGAGCGCGGTGCGCGCGCATGTGCGATC 375  
 DB 301 CTGGCGGCTATCGTGGCGCGCGCGAGAGCGCGGTGCGCGCGCATGTGCGATC 360  
 QY 376 CTGATTTGGAACCCCAACGAGAGCGCGTGAAGGATCCGCGCTTGGAGAACTCAGCGTG 435  
 DB 361 CTGATTTGGAACCCCAACGAGAGCGCGTGAAGGATCCGCGCTTGGAGAACTCAGCGTG 420  
 QY 436 TTTTGGAGAGAGCGCGCAGCGCTTAAAGACTGGGTGCCAGCATCACTCCCGAG 492  
 DB 421 TTTTGGAGAGAGCGCGCAGCGCTTAAAGACTGGGTGCCAGCATCACTCCCGAG 477

RESULT 14  
 US-08-463-074B-31  
 ; Sequence 31, Application US/08463074B  
 ; Patent No. 6020155  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Smith, Kendall A. & Beadling, Carol  
 ; TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an  
 ; NUMBER OF SEQUENCES: 35  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0,  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/463,074B  
 ; FILING DATE: 5-JUN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/104,736  
 ; FILING DATE: 10-AUG-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/796,066  
 ; FILING DATE: 20-NOV-91  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Viviana Amzel, Ph. D.  
 ; REGISTRATION NUMBER: 30,930  
 ; REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-4210  
 ; TELEFAX: (213) 489-4210  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 477 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA

1-463-074B-31

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Query Match      86.6%; Score 477; DB 3; Length 477;
Query Local Similarity 100.0%; Pred. No. 1.5e-100;
Query Mismatches 477; Conservative 0; Indels 0; Gaps 0;

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196 GTCTCGGCTCCGGGTGAGAGAGACAGAGGCGACATCCGCGTCGACATCAATTTTACGCTG 255  
181 GTCTCGGCTCCGGGTGAGAGAGACAGAGGCGACATCCGCGTCGACATCAATTTTACGCTG 240  
256 ATCCAGGCTTTCTGCTCCGAGAACGACATGACATAGTGGCGCTGGGCGCATGTGACAGCG 315  
241 ATCCAGGCTTTCTGCTCCGAGAACGACATGACATAGTGGCGCTGGGCGCATGTGACAGCG 300  
316 CTGAGCGGCTATCGTGGGCGCGCGCGAGAGAGCGCGGTCGCGCGGCGACCTGCACTGCATC 375  
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361 CTCAATTTGGAACCCCAACGAGACGCTGGAAGATCCCGCTTTGGAGAAAGCTCAGCTTG 420  
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421 TTTTGGAGAGAGCGGACAGCTTAAAGACATGGGTGCGACAGATCACTCCCGAG 477

T 15  
 1-465-585C-31  
 Invention 31, Application US/08465585C  
 ent No. 6027914  
 GENERAL INFORMATION:  
 APPLICANT: Smith, K. A., & Beadling, C.  
 TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector  
 TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: PRETTY, SCHROEDER & POPLAWSKI  
 ADDRESSEE: (B) STREET:  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 900071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/465,585C  
 FILING DATE: 5-JUNE-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/330,108  
 FILING DATE: 27-OCT-1994  
 APPLICATION NUMBER: USSN 08/104,736  
 FILING DATE: 10-AUG-1993  
 APPLICATION NUMBER: USSN 07/796,066  
 FILING DATE: 20-NOV-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930

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? REFERENCE/DOCKET NUMBER: P66 38149 (DART-0500)
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 622-7700
? TELEFAX: (213) 4894210
? INFORMATION FOR SEQ ID NO: 31:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 477 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA
? US-08-465-585C-31

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Query Match	86.6%;	Score 477;	DB 3;	Length 477;
Best Local Similarity	100.0%;	Pred. No. 1.5e-100;		
Matches 477;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db	61	GGTGC CGG GAAAGCGCTGCATGAGTTGCTGTGTGGGGCAGCGCTCAGGGCTGCGCTCACT	120
OY	136	GCCGCGCGTCTACGAGTCAAGCCAAATCTTTGAACGTTGGAACCCCGGACAAATGTGAACCTTCTGT	195
Db	121	GCCGCGCGTCTACGAGTCAAGCCAAATCTTTGAACGTTGGAACCCCGGACAAATGTGAACCTTCTGT	180
OY	196	GTGCTGCGCTGCGGGTGAAGAGACGAGGGCGCATTCGCGCTTSCAGATCCATTTTAAAGCTTG	255
Db	181	GTGCTGCGCTGCGGGTGAAGAGACGAGGGCGCATTCGCGCTTSCAGATCCATTTTAAAGCTTG	240
OY	256	ATCCAGAGCTTTTCTGCTGCAGAGAACCACTATCAATATGTGCGGCTGGGCGCATGTGCAGCGG	315
Db	241	ATCCAGAGCTTTTCTGCTGCAGAGAACCACTATCAATATGTGCGGCGCATGTGCAGCGG	300
OY	316	CTGGCGCGCTATTCGTGGGCGCGCGCAGAGAGCGGGTGCAGCCGGCGCATCTGCATCTCATC	375
Db	301	CTGGCGCGCTATTCGTGGGCGCGCGCAGAGAGCGGGTGCAGCCGGCGCATCTGCATCTCATC	360
OY	376	CTCATTTTGCAAACCCCAACAGAGACGCTCTGAAGATCCCGCTTTGGAGAAAGCTCAAGCTTG	435
Db	361	CTCATTTTGCAAACCCCAACAGAGACGCTCTGAAGATCCCGCTTTGGAGAAAGCTCAAGCTTG	420
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Search completed: June 4, 2006, 22:37:55  
Job time : 176 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

nucleic - nucleic search, using sw model

June 4, 2006, 22:27:39 ; Search time 1111 Seconds  
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IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

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processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

base : Published Applications NA Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
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- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11E\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Query	Match	Length	ID	Description
1	542	98.4	1056	US-10-821-234-275
2	542	98.4	1065	US-09-879-833-1
3	542	98.4	1066	US-10-287-436A-712
4	542	98.4	1078	US-10-263-310-9
5	542	98.4	1078	US-10-172-118-1310
6	542	98.4	1078	US-10-342-887-1310
7	542	98.4	1078	US-10-626-905-9
8	542	98.4	1078	US-10-278-698-221
9	542	98.4	1078	US-10-278-698-736
10	542	98.4	1078	US-10-287-436A-86
11	542	98.4	1078	US-10-631-467-37
12	527.8	95.8	750	US-10-641-643-820
13	525.4	95.4	612	US-10-723-860-3639
14	512.8	93.1	1202	US-10-723-860-7602
15	477	86.6	1302	US-10-087-192-1355
16	431.4	78.3	1077	US-10-764-420-7
17	431.4	78.3	1084	US-10-263-330-11

18	431.4	78.3	1084	US-10-626-905-11	Sequence 11, Appl
19	431.4	78.3	1084	US-10-631-467-965	Sequence 965, App
20	423.6	76.9	1073	US-10-087-192-1352	Sequence 1352, Ap
21	278.8	50.6	344	US-10-617-316-45	Sequence 45, Appl
22	274	49.7	444	US-09-879-833-3	Sequence 3, Appl
23	274	49.7	21543	US-10-087-192-1354	Sequence 1354, Ap
24	187	33.9	21795	US-10-087-192-1351	Sequence 1351, Ap
25	180.4	32.7	483	US-10-821-234-453	Sequence 453, App
26	180.4	32.7	1378	US-10-278-698-220	Sequence 220, App
27	180.4	32.7	1378	US-10-278-698-735	Sequence 735, App
28	168	30.5	1305	US-10-263-330-3	Sequence 3, Appl
29	168	30.5	1305	US-10-626-905-3	Sequence 2414, Ap
30	159.4	28.9	1121	US-10-263-330-1	Sequence 1, Appl
31	159.4	28.9	1121	US-10-626-905-1	Sequence 1, Appl
32	159.4	28.9	1121	US-10-626-905-1	Sequence 219, App
33	159.4	28.9	1121	US-10-626-905-1	Sequence 734, App
34	159.4	28.9	1121	US-10-278-698-734	Sequence 1020, Ap
35	157.2	28.5	1242	US-11-128-061-1020	Sequence 4662, Ap
36	157.2	28.5	1242	US-11-128-061-1020	Sequence 1020, Ap
37	157.2	28.5	1242	US-11-128-049-4662	Sequence 4662, Ap
38	157.2	28.5	1242	US-10-278-698-217	Sequence 217, App
39	154.4	28.0	998	US-10-278-698-732	Sequence 732, App
40	154.4	28.0	1343	US-09-880-107-2368	Sequence 2368, Ap
41	154.4	28.0	1343	US-10-641-643-1085	Sequence 1085, Ap
42	154.4	28.0	1343	US-10-278-698-216	Sequence 216, App
43	154.4	28.0	1343	US-10-278-698-731	Sequence 731, App
44	154.4	28.0	1343	US-10-278-698-731	Sequence 5, Appl
45	154.4	28.0	1355	US-10-263-330-5	

# ALIGNMENTS

RESULT 1  
US-10-821-234-275/c  
Sequence 275, Application US/10821234  
Publication No. US0050255114A1  
GENERAL INFORMATION:  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Andarmant, Susan  
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
FILE REFERENCE: 821A  
CURRENT APPLICATION NUMBER: US/10/821,234  
CURRENT FILING DATE: 2004-04-07  
PRIOR APPLICATION NUMBER: US 60/462,047  
PRIOR FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 1704  
SOFTWARE: pt\_seq\_genes Version 1.0  
SEQ ID NO 275  
LENGTH: 1056  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-821-234-275

Query Match	98.4%	Score 542;	DB 10;	Length 1056;
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920	ACACCGAGATGACGAGTGCAGGAAAGCGCTGATAGTTGCTGCGGACAGCT	861		
121	CAGGCTGCTCACTGCGGCGTTTACGAGTCAACCAAGTTTGAACGTGACCCGAC	180		
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181	AATGTGACCTTCTGTGTGCTGCTGCGGAGTGAAGAGACGAGGCGACATCGCGTGCAG	240		

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 241 ATTCATTTTACGCTGATCCAGGCTTTTCTGCTCGAGAACGCAATGACATATGTCGCGT 300  
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879-833-1  
 plence 1, Application US/09879833  
 ent No. US20020055107A1  
 ERAL INFORMATION:  
 PPLICANT: Park, Chong-Hun; SAMYANG GENEX CORPORATION  
 TLE OF INVENTION: CANCER DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL DIFFERENTIATION  
 TLE OF INVENTION: FERMENTATION SPECIFIC SYG972 GENE AND GENOMIC DNA AND PROMOTER T  
 TLE OF INVENTION: ERROR  
 LE REFERENCE: PA/SYG/99601  
 RRENT APPLICATION NUMBER: US/09/879, 833  
 RRENT FILING DATE: 2001-06-12  
 IOR APPLICATION NUMBER: KR 54933  
 IOR FILING DATE: 1998-12-12  
 IOR APPLICATION NUMBER: KR 63958  
 IOR FILING DATE: 1998-12-30  
 MBER OF SEQ ID NOS: 3  
 FTWARE: KOPATIN 1.5  
 ID NO 1  
 LENGTH: 1066  
 TYPE: DNA  
 ORGANISM: HL60 cell line  
 879-833-1

98.4%; Score 542; DB 3; Length 1066;  
 Local Similarity 100.0%; Pred. No. 4.5e-150;  
 ches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 61 ACAGCAGAGATGCAAGGTGCGCGGAAAGCGCTGACATGATGCTGTGCGCGAGCGT 120  
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 181 AATGTCACCTTTGTGTGCTGCTGCGGCTGAGAGAGACGAGGGGCGACATCGCGTGCAG 240  
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 241 ATTCATTTTACGCTGATCCAGGCTTTTCTGCTCGAGAACGCAATGACATATGTCGCGGT 300

Db	323	ATCCATTTTACGCTGATCCAGGCTTTCTGCTGCGAAGACGATCGACATGATGCGCGTG	382
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Db	443	GACCTGCAGCTGCATCTCATTTGCAACCCCAACGAGAGACGCTGGAAAGATCCCGGCTTG	502
Qy	421	GAGAACTCAGGCTGTTTTCGAGAGAGACCGCAGCGTTTAACGACTGGTGCCACGATC	480
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RESULT 3
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; Sequence 712, Application US//10287436A
; Publication No. US2005020421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872, 514696
; CURRENT APPLICATION NUMBER: US/10/287, 436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 712
; LENGTH: 1066
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-287-436A-712

Query Match      98.4%; Score 542; DB 10; Length 1066;
Best Local Similarity 100.0%; Pred. No. 4,5e-150;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      121      CAGGGCTGCTCATCTGCGCGCGGTCTACAGAGTCAGACCAAGCTTGAACGTGAGACCCCGAC 180
QY      203      CAGGGCTGCTCATCTGCGCGCGGTCTACAGAGTCAGACCAAGCTTGAACGTGAGACCCCGAC 262
Db      181      AATGAGACCTTCTGTGTGCTGTGGTGGCGGTGAGGAGGACGAGGGGCGACATCGCGCTGAG 240
QY      263      AATGAGACCTTCTGTGTGCTGTGGTGGCGGTGAGGAGGACGAGGGGCGACATCGCGCTGAG 322
Db      241      ATCCATTTTACGCTGATCCAGGCTTTTGTCTGCGAGAAACGACATGACATGATAGTGGCGTG 300
QY      323      ATCCATTTTACGCTGATCCAGGCTTTTGTCTGCGAGAAACGACATGACATGATAGTGGCGTG 382
Db      301      GCGCATGTGACGCGGCTGGCGGCTATCTGTGGGCGCGCGGCGAGGAGCGCGGTGCGCGGGGC 360
QY      383      GCGCATGTGACGCGGCTGGCGGCTATCTGTGGGCGCGCGGCGAGGAGCGCGGTGCGCGGGGC 442

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361 GACCTGACATGATCTCTATTTGAAACCCCAAGAGAGCCCTGGAAGATCCCGCTTG 420  
 443 GACCTGACATGATCTCTATTTGAAACCCCAAGAGAGCCCTGGAAGATCCCGCTTG 502  
 421 GAGAGCTGACCTGTTTGGGAGAGAGCCCGAGTTTAAAGATGCTGGTCCCAATC 480  
 503 GAGAGCTGACCTGTTTGGGAGAGAGCCCGAGTTTAAAGATGCTGGTCCCAATC 562  
 481 ACCCTCCGAGTGAAGAGCCCGAGGAGCTTGTCTGATGAGCTGGTGAAGCCCGG 540  
 563 ACCCTCCGAGTGAAGAGCCCGAGGAGCTTGTCTGATGAGCTGGTGAAGCCCGG 622  
 541 GG 542  
 623 GG 624

1.7 4  
 0-263-330-9  
 nence 9, Application US/1026330  
 ublication No. US20030077262A1  
 IERAL INFORMATION:  
 PPLICANT: FRANZOSO, GUIDO  
 PPLICANT: DESMALE, ENRICO  
 PPLICANT: ZAZZERONI, FRANCESCA  
 PPLICANT: PAPA, SALVATORE  
 TLE OF INVENTION: MODULATORS OF APOPTOSIS  
 LE REFERENCE: ARCD:379USPI  
 RRENT APPLICATION NUMBER: US/10/263,330  
 RRENT FILING DATE: 2002-10-02  
 RIOR APPLICATION NUMBER: US/60/326,492  
 RIOR FILING DATE: 2001-10-02  
 UMBER OF SEQ ID NOS: 15  
 FTWARE: PatentIn Ver. 2.1  
 ? ID NO 9  
 LENGTH: 1078  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 0-263-330-9

Query Match 98.4%; Score 542; DB 6; Length 1078;  
 nt Local Similarity 100.0%; Pred. No. 4.5e-150;  
 tches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CTGGTTGATGCACTATGACTCTGGAAGAAATCCGCGCCAGAGACAGATTCCGAAAGC 60  
 95 CTGGTTGATGCACTATGACTCTGGAAGAAATCCGCGCCAGAGACAGATTCCGAAAGC 154  
 61 ACAGCCAGATGCAAGGAGTCCGGGAAAGCGCTGATGATTGCTGTCGGCGACGCT 120  
 155 ACAGCCAGATGCAAGGAGTCCGGGAAAGCGCTGATGATTGCTGTCGGCGACGCT 214  
 121 CAGGGCTGCTCACTGCGCGGCTTACAGATCAAGCAAGCTTGAACGTGGAACCCGAC 180  
 215 CAGGGCTGCTCACTGCGCGGCTTACAGATCAAGCAAGCTTGAACGTGGAACCCGAC 274  
 181 AATGTGACCTTCTGTGTGCTGCGGAGTGAAGAGACGAGGCGCATGCGCTGAG 240  
 275 AATGTGACCTTCTGTGTGCTGCGGAGTGAAGAGACGAGGCGCATGCGCTGAG 334  
 241 ATCCATTTTACGCTGATCCAGGCTTTCTGCTGAGAAAGCATGACATAGTGGCGTG 300  
 335 ATCCATTTTACGCTGATCCAGGCTTTCTGCTGAGAAAGCATGACATAGTGGCGTG 394  
 301 GGGATGTGACGCGGCTGCGGCTATGATGCGGCGCGCGAGAGGCGGGTGGCGCGGC 360  
 395 GGGATGTGACGCGGCTGCGGCTATGATGCGGCGCGCGAGAGGCGGGTGGCGCGGC 454  
 361 GACCTGACATGATCTCTATTTGAAACCCCAAGAGAGCCCTGGAAGATCCCGCTTG 420  
 455 GACCTGACATGATCTCTATTTGAAACCCCAAGAGAGCCCTGGAAGATCCCGCTTG 514  
 421 GAGAGCTGACCTGTTTGGGAGAGAGCCCGAGTTTAAAGATGCTGGTCCCAATC 480

Db 515 GAGAGCTGACCTGTTTGGGAGAGAGCCCGAGTTTAAAGATGCTGGTCCCAATC 574  
 QY 481 ACCCTCCGAGTGAAGAGCCCGAGGAGCTTGTCTGATGAGCTGGTGAAGCCCGG 540  
 Db 575 ACCCTCCGAGTGAAGAGCCCGAGGAGCTTGTGTGATGAGCTGGTGAAGCCCGG 634  
 QY 541 GG 542  
 Db 635 GG 636

RESULT 5  
 US-10-172-118-1310  
 ; Sequence 1310, Application US/10172118  
 ; Publication No. US20030224374A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dai, Hongyue  
 ; APPLICANT: He, Yundong  
 ; APPLICANT: Linsley, Peter  
 ; APPLICANT: Mao, Mao  
 ; APPLICANT: Roberts, Chris  
 ; APPLICANT: Van 't Veer, Laura  
 ; APPLICANT: Van de Vijver, Marc  
 ; APPLICANT: Bernards, Rene  
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
 ; FILE REFERENCE: 9301-175-999  
 ; CURRENT APPLICATION NUMBER: US/10/172,118  
 ; CURRENT FILING DATE: 2002-06-14  
 ; PRIOR APPLICATION NUMBER: 60/380,770  
 ; PRIOR FILING DATE: 2002-05-14  
 ; NUMBER OF SEQ ID NOS: 2699  
 ; SEQ ID NO 1310  
 ; LENGTH: 1078  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; PUBLICATION INFORMATION:  
 ; DATABASE ACCESSION NUMBER: NM\_006705  
 ; DATABASE ENTRY DATE: 2001-06-18  
 ; US-10-172-118-1310

Query Match 98.4%; Score 542; DB 7; Length 1078;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-150;  
 Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CTGGTTGATGCACTATGACTCTGGAAGAAATCCGCGCCAGAGACAGATTCCGAAAGC 60  
 95 CTGGTTGATGCACTATGACTCTGGAAGAAATCCGCGCCAGAGACAGATTCCGAAAGC 154  
 61 ACAGCCAGATGCAAGGAGTCCGGGAAAGCGCTGATGATTGCTGTCGGCGACGCT 120  
 155 ACAGCCAGATGCAAGGAGTCCGGGAAAGCGCTGATGATTGCTGTCGGCGACGCT 214  
 121 CAGGGCTGCTCACTGCGCGGCTTACAGATCAAGCAAGCTTGAACGTGGAACCCGAC 180  
 215 CAGGGCTGCTCACTGCGCGGCTTACAGATCAAGCAAGCTTGAACGTGGAACCCGAC 274  
 181 AATGTGACCTTCTGTGTGCTGCGGAGTGAAGAGACGAGGCGCATGCGCTGAG 240  
 275 AATGTGACCTTCTGTGTGCTGCGGAGTGAAGAGACGAGGCGCATGCGCTGAG 334  
 241 ATCCATTTTACGCTGATCCAGGCTTTCTGCTGAGAAAGCATGACATAGTGGCGTG 300  
 335 ATCCATTTTACGCTGATCCAGGCTTTCTGCTGAGAAAGCATGACATAGTGGCGTG 394  
 301 GGGATGTGACGCGGCTGCGGCTATGATGCGGCGCGCGAGAGGCGGGTGGCGCGGC 360  
 395 GGGATGTGACGCGGCTGCGGCTATGATGCGGCGCGCGAGAGGCGGGTGGCGCGGC 454  
 361 GACCTGACATGATCTCTATTTGAAACCCCAAGAGAGCCCTGGAAGATCCCGCTTG 420  
 455 GACCTGACATGATCTCTATTTGAAACCCCAAGAGAGCCCTGGAAGATCCCGCTTG 514

421	GAAAGATCGACCGCTGTTTTCGAGGAGAGCGGAGCGTTTAA	CGACTGGGTCACCATTC	480
515	GAGAACTCAGCCTCTGTTTTCGAGAGAGCGCGACGTTAC	CACTGGGTGCCACATTC	574
481	ACCCCTCCCGAGTGACAGCCCGGCGGACCTTGCTGATCG	ACGTGTGACGCCCGG	540
575	ACCCCTCCCGAGTGACAGCCCGGCGGAGCCTTGCTGATCG	ACGTGTGACGCCCGG	634
541	GG	542	
635	GG	636	
T 6			
1-342-887-1310			
quence 1310, Application US/10342887			
lication No. US20040058340A1			
ERAL INFORMATION:			
PLICANT: Dai, Hongyue			
PLICANT: He, Yudong			
PLICANT: Linsley, Peter S.			
PLICANT: Mao, Mao			
PLICANT: Roberts, Christopher J.			
PLICANT: Van 't Veer, Laura Johanna			
PLICANT: Van de Vijver, Marc J.			
PLICANT: Bernards, Rene			
TE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients			
RE REFERENCE: 9301-188-999			
RENT APPLICATION NUMBER: US/10/342,887			
RENT FILING DATE: 2003-01-15			
OR APPLICATION NUMBER: 60/298,918			
OR FILING DATE: 2001-06-18			
OR APPLICATION NUMBER: 60/380,710			
OR FILING DATE: 2002-05-14			
OR APPLICATION NUMBER: 10/172,118			
OR FILING DATE: 2002-06-14			
MBER OF SEQ ID NOS: 2699			
ID NO 1310			
LENGTH: 1078			
TYPE: DNA			
RGANISM: Homo sapiens			
1-342-887-1310			
RY Match	98.4%	Score 542;	DB 8; Length 1078;
ct Local Similarity	100.0%;	Pred. No. 4.5e-150;	
ches 542; Conservative	0;	Mismatches	0; Indels
			Gaps
1	CTGGTTGATCGCACTATGACTCTGTGAGAGAGTCCGCGGCGCAGACACACAGTTCCGAAAGC	60	
95	CTGGTTATGCACTATGACTCTGTGAGAGAGTCCGCGGCGCAGACACAGTTCCGAAAGC	154	
61	ACAGCCAGATGCAAGGGTGC CGGAAAGCGCTGATGATGTTGCTGTGCGCGCAGCGT	120	
155	ACAGCCAGATGCAAGGGTGC CGGAAAGCGCTGATGATGTTGCTGTGCGCGCAGCGT	214	
121	CAGGGCTGCTCATCTGCGCGGCGTTAAGAGTCAGCCAAAGCTTTGAACGTGACCCCGAC	180	
215	CAGGGCTGCTCATCTGCGCGGCGTTAAGAGTCAGCCAAAGCTTTGAACGTGACCCCGAC	274	
181	AATGTGACCTTCTGTGCTGCTGCGGAGTGAGGAGACGAGGCGCATTCGCGCTCAG	240	
275	AATGTGACCTTCTGTGCTGCTGCGGAGTGAGGAGACGAGGCGCATTCGCGCTCAG	334	
241	ATCCATTTTACGCTGATCCAGGCTTTTCTGCTGCGAGAACGACATTCAGTATGCGCGTG	300	
335	ATCCATTTTACGCTGATCCAGGCTTTTCTGCTGCGAGAACGACATTCAGTATGCGCGTG	394	
301	GGCGATGTGACGCGGCTGCGCGCTATGTGTGGCCCGCGAGAGCGGGTGC CGCGGC	360	
395	GGCGATGTGACGCGGCTGCGCGCTATGTGTGGCCCGCGAGAGCGGGTGC CGCGGC	454	
361	GACCTGCATGCATTCCTCATTTTGAACCCCAAGAGACGCTGTGAGAGATCCCGCGCTTG	420	

Db	455	GACCTGCAC	TGCATCTCATTTCCAA	CCCCAACGAGACGCGCTGGAAGATCCCGCCTTG	514
QY	421	GAGAA	GCTCAGCCTGTTT	TGGAGAGAAAGCCGCGACGCTTAA	CGATCGTGGTCCAGATC 480
Db	515	GAGAA	GCTCAGCCTGTTT	TGGAGAGAAAGCCGCGACGCTTAA	CGATCGTGGTCCAGATC 574
QY	481	ACCC	TCCCGCAGTACAC	CCCGCGGGGAACTTGTGTGATCGACGTGTGACCGCCCGG	540
Db	575	ACCC	TCCCGCAGTACAC	CCCGCGGGGAACTTGTGTGATCGACGTGTGACCGCCCGG	634
QY	541	GG	542		
Db	635	GG	636		
RESULT 7					
US-10-626-905-9					
; Sequence 9, Application US/10626905					
; Publication No. US20040121463A1					
GENERAL INFORMATION:					
APPLICANT: FRANZOSE, GUIDO					
APPLICANT: DESMAELE, ENRICO					
APPLICANT: ZAZZERONI, FRANCESCA					
APPLICANT: PAPA, SALVATORE					
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS					
FILE REFERENCE: 21459-94575					
CURRENT APPLICATION NUMBER: US/10/626,905					
CURRENT FILING DATE: 2003-07-25					
PRIOR APPLICATION NUMBER: PCT/US02/31548					
PRIOR FILING DATE: 2002-10-02					
PRIOR APPLICATION NUMBER: 10/263,330					
PRIOR FILING DATE: 2002-10-02					
PRIOR APPLICATION NUMBER: 60/328,811					
PRIOR FILING DATE: 2001-10-12					
PRIOR APPLICATION NUMBER: 60/326,492					
PRIOR FILING DATE: 2001-10-02					
NUMBER OF SEQ ID NOS: 53					
SOFTWARE: PatentIn Ver. 3.2					
SEQ ID NO 9					
LENGTH: 1078					
TYPE: DNA					
ORGANISM: Homo sapiens					
US-10-626-905-9					
Query Match 98.4%; Score 542; DB 8; Length 1078;					
Best Local Similarity 100.0%; Pred. No. 4.3e-150;					
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0.					





```

T 10
-287-436A-86
nuence 86, Application US/10287436A
lication No. US2005020421A1
ERAL INFORMATION:
PLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
TLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
LE OF INVENTION: RHEUMATOID ARTHRITIS
LE REFERENCE: 10872.514696
RRENT APPLICATION NUMBER: US/10/287,436A
RRENT FILING DATE: 2002-10-31
IOR APPLICATION NUMBER: US 60/336,220
IOR FILING DATE: 2001-10-31
MBER OF SEQ ID NOS: 1446
FTWARE: FastSeq for windows Version 4.0
: ID NO 86
NGTH: 1078
YPE: DNA
GANISM: Homo sapiens
-287-436A-86

-ry Match          98.4%; Score 542; DB 10; Length 1078;
: Local Similarity 100.0%; Pred. No. 4.5e-150;
ches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGGTTGATGCACTATGACTCTGGAAGATCCGGCGCCAGACACAGTTCCGGAAGC 60
|||
95 CTGGTTGATGCACTATGACTCTGGAAGATCCGGCGCCAGACACAGTTCCGGAAGC 154
|||
61 ACAGCCAGATGAGGAGGTCGGGAAAGCGCTGATGAGTTGCTGCTGTCGGCGACGCT 120
|||
155 ACAGCCAGATGAGGAGGTCGGGAAAGCGCTGATGAGTTGCTGCTGTCGGCGACGCT 214
|||
121 CAGGGCTGCTCACTGCGCGCTCTAAGAGTCAGCCAAAGCTTTGAACGTGACCCGAC 180
|||
215 CAGGGCTGCTCACTGCGCGCTCTAAGAGTCAGCCAAAGCTTTGAACGTGACCCGAC 274
|||
181 AATGTACCTTCTGTGTGCTGCTGCGGAGGAGAGAGAGGAGGAGGAGGAGGAGGAG 240
|||
275 AATGTACCTTCTGTGTGCTGCTGCGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAG 334
|||
241 ATTCATTTTACGCTGATCCAGGCTTCTGCTGCGAGAGACATCGACATAGTGCAGTG 300
|||
335 ATTCATTTTACGCTGATCCAGGCTTCTGCTGCGAGAGACATCGACATAGTGCAGTG 394
|||
301 GGGGATGTGACAGCGGCTGCGGCTATCGTGAGGCGCGGCGAGAGGCGGAGTGCAGGCG 360
|||
395 GGGGATGTGACAGCGGCTGCGGCTATCGTGAGGCGCGGCGAGAGGCGGAGTGCAGGCG 454
|||
361 GACCTGCACTGCACTCTCATTTTGAACCCCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 420
|||
455 GACCTGCACTGCACTCTCATTTTGAACCCCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 514
|||
421 GAGAGCTCAGCTGTTTTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
|||
515 GAGAGCTCAGCTGTTTTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 574
|||
481 ACCCTCCCGAGTGAAGCCCGGCGGAGCTTGTGTGATCGACGTGTGACGCCCGG 540
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575 ACCCTCCCGAGTGAAGCCCGGCGGAGCTTGTGTGATCGACGTGTGACGCCCGG 634
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541 GG 542
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635 GG 636

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; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: Patentrln version 3.1
; SEQ ID NO 37
; LENGTH: 1078
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-631-467-37

Query Match          98.4%; Score 542; DB 10; Length 1078;
Best Local Similarity 100.0%; Pred. No. 4.5e-150;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGGTTGATGCACTATGACTCTGGAAGATCCGGCGCCAGACACAGTTCCGGAAGC 60
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DB 95 CTGGTTGATGCACTATGACTCTGGAAGATCCGGCGCCAGACACAGTTCCGGAAGC 154
|||
QY 61 ACAGCCAGATGAGGAGGTCGGGAAAGCGCTGATGAGTTGCTGCTGTCGGCGACGCT 120
|||
DB 155 ACAGCCAGATGAGGAGGTCGGGAAAGCGCTGATGAGTTGCTGCTGTCGGCGACGCT 214
|||
QY 121 CAGGGCTGCTCACTGCGCGCTCTAAGAGTCAGCCAAAGCTTTGAACGTGACCCGAC 180
|||
DB 215 CAGGGCTGCTCACTGCGCGCTCTAAGAGTCAGCCAAAGCTTTGAACGTGACCCGAC 274
|||
QY 181 AATGTACCTTCTGTGTGCTGCTGCGGAGGAGAGAGAGGAGGAGGAGGAGGAGGAG 240
|||
DB 275 AATGTACCTTCTGTGTGCTGCTGCGGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAG 334
|||
QY 241 ATTCATTTTACGCTGATCCAGGCTTCTGCTGCGAGAGACATCGACATAGTGCAGTG 300
|||
DB 335 ATTCATTTTACGCTGATCCAGGCTTCTGCTGCGAGAGACATCGACATAGTGCAGTG 394
|||
QY 301 GGGGATGTGACAGCGGCTGCGGCTATCGTGAGGCGCGGCGAGAGGCGGAGTGCAGGCG 360
|||
DB 395 GGGGATGTGACAGCGGCTGCGGCTATCGTGAGGCGCGGCGAGAGGCGGAGTGCAGGCG 454
|||
QY 361 GACCTGCACTGCACTCTCATTTTGAACCCCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 420
|||
DB 455 GACCTGCACTGCACTCTCATTTTGAACCCCAAGAGAGAGGAGGAGGAGGAGGAGGAGGAG 514
|||
QY 421 GAGAGCTCAGCTGTTTTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
|||
DB 515 GAGAGCTCAGCTGTTTTCGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 574
|||
QY 481 ACCCTCCCGAGTGAAGCCCGGCGGAGCTTGTGTGATCGACGTGTGACGCCCGG 540
|||
DB 575 ACCCTCCCGAGTGAAGCCCGGCGGAGCTTGTGTGATCGACGTGTGACGCCCGG 634
|||
QY 541 GG 542
||
DB 635 GG 636

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RESULT 12

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US-10-641-643-820
; Sequence 820, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Suan G. Stuart
; Jeffrey J. Sellhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/641,643  
FILING DATE: 14-Aug-2003  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 820:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 750 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

IMMEDIATE SOURCE:  
LIBRARY: PROSTUT04  
CLONE: 828764

SEQUENCE DESCRIPTION: SEQ ID NO: 820 :  
0-641-643-820

Query Match 95.4%; Score 527.8; DB 8; Length 750;  
Best Local Similarity 99.4%; Pred. No. 7e-146;  
Matches 540; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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1 CTGGTGTATGCACTATGACTCTGGAAGAAAGTCCGCGCCAGAGACAGATTCCGGAAGC 60
84 CTGGTGTATGCACTATGACTCTGGAAGAAAGTCCGCGCCAGAGACAGATTCCGGAAGC 143
61 ACAGCCAGATGAGAGGAGTCCGGGAAAGCCCTGATGATGTTGCTGCGGCGCAGCGT 120
144 ACAGCCAGATGAGAGGAGTCCGGGAAAGCCCTGATGATGTTGCTGCGGCGCAGCGT 203
121 CAGGGCTGCTCACTGCGCGGCTTACAGATCAAGCCAAAGTCTTGAACGTGACCCCGAC 180
204 CAGGGCTGCTCACTGCGCGGCTTACAGATCAAGCCAAAGTCTTGAACGTGACCCCGAC 263
181 AATGTGACCTTCTGTGTGCTGCTGCGGAGTGAAGAGACAGAGGCGCATCGCCCTGAG 240
264 AATGTGACCTTCTGTGTGCTGCTGCGGAGTGAAGAGACAGAGGCGCATCGCCCTGAG 323
241 ATCATTTTACGCTGATCCAGGCTTTTCTGCTGCGAGAACGATCGACATAGTGGCGTG 300
324 ATCATTTTACGCTGATCCAGGCTTTTCTGCTGCGAGAACGATCGACATAGTGGCGTG 383
301 GGCATGTGACGCGGCTGCGGCTATGCTGCGCGCCGCGAGAGAGCGGCTGCGCCGCGC 360
384 GGCATGTGACGCGGCTGCGGCTATGCTGCGCGCCGCGAGAGAGCGGCTGCGCCGCGC 443
361 GACCTGACATGCACTCTCATTTTGAACCCCAAGAGAGAGCGCTT-GAAGAGATCCCGCTT 419
444 GACCTGACATGCACTCTCATTTTGAACCCCAAGAGAGAGCGCTTGAAGAGATCCCGCTT 503
420 GAGAGAGCTGAGCTGTTTTCGAGAGAGAGCGGAGCGTTAAGCACTGGGTGCCAGCAT 479
504 GAGAGAGCTGAGCTGTTTTCGAGAGAGAGCGGAGCGTTAAGCACTGGGTGCCAGCAT 563

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QY 480 CACCTTCCCGAGTGAACAGCCCGCGGAGACCTTGTCTGATGACAGTGTGACGCCCGC 539
DB 564 CACCTTCCCGAGTGAACAGCCCGCGGAGACCTTGTCTGATGACAGTGTGACGCCCGC 623
QY 540 GGG 542
DB 624 GGG 626

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RESULT 13  
US-10-723-860-3639  
Sequence 3639, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsburg, Wendy M.  
TITLE OF INVENTION: Methods of diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
FILE REFERENCE: 05882.0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
CURRENT FILING DATE: 2003-11-26  
PRIOR APPLICATION NUMBER: 60/429,739  
PRIOR FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3639  
LENGTH: 612  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-723-860-3639

Query Match 95.4%; Score 525.4; DB 9; Length 612;  
Best Local Similarity 99.8%; Pred. No. 3.5e-145;  
Matches 526; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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1 CTGGTGTATGCACTATGACTCTGGAAGAAAGTCCGCGCCAGAGACAGATTCCGGAAGC 60
86 CTGGTGTATGCACTATGACTCTGGAAGAAAGTCCGCGCCAGAGACAGATTCCGGAAGC 145
61 ACAGCCAGATGAGAGGAGTCCGGGAAAGCCCTGATGATGTTGCTGCGGCGCAGCGT 120
146 ACAGCCAGATGAGAGGAGTCCGGGAAAGCCCTGATGATGTTGCTGCGGCGCAGCGT 205
121 CAGGGCTGCTCACTGCGCGGCTTACAGATCAAGCCAAAGTCTTGAACGTGACCCCGAC 180
206 CAGGGCTGCTCACTGCGCGGCTTACAGATCAAGCCAAAGTCTTGAACGTGACCCCGAC 265
181 AATGTGACCTTCTGTGTGCTGCTGCGGAGTGAAGAGACAGAGGCGCATCGCGCTGAG 240
266 AATGTGACCTTCTGTGTGCTGCTGCGGAGTGAAGAGACAGAGGCGCATCGCGCTGAG 325
241 ATCATTTTACGCTGATCCAGGCTTTTCTGCTGCGAGAACGATCGACATAGTGGCGTG 300
326 ATCATTTTACGCTGATCCAGGCTTTTCTGCTGCGAGAACGATCGACATAGTGGCGTG 385
301 GGCATGTGACGCGGCTGCGGCTATGCTGCGCGCCGCGAGAGAGCGGCTGCGCCGCGC 360
386 GGCATGTGACGCGGCTGCGGCTATGCTGCGCGCCGCGAGAGAGCGGCTGCGCCGCGC 445
361 GACCTGACATGCACTCTCATTTTGAACCCCAAGAGAGAGCGCTTGAAGAGATCCCGCTT 420
446 GACCTGACATGCACTCTCATTTTGAACCCCAAGAGAGAGCGCTTGAAGAGATCCCGCTT 505
421 GAGAGAGCTGAGCTGTTTTCGAGAGAGAGCGGAGCGTTAAGCACTGGGTGCCAGCATC 480
506 GAGAGAGCTGAGCTGTTTTCGAGAGAGAGCGGAGCGTTAAGCACTGGGTGCCAGCATC 565
481 ACCCTCCCGAGTGAACAGCCCGCGGAGAGCGTTGTTGATCGACGT 527
566 ACCCTCCCGAGTGAACAGCCCGCGGAGAGCGTTGTTGATCGACGT 612
DB

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T 14  
-723-860-7602  
Invention 7602, Application US/10723860  
Publication No. US20040253606A1  
GENERAL INFORMATION:  
APPLICANT: Atiz, Natasha  
APPLICANT: Ginsburg, Wendy M.  
INVENTOR: Zlotnick, Albert  
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
METHODS OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
LE REFERENCE: 05882.0193.NPUS01  
CURRENT APPLICATION NUMBER: US/10/723,860  
PRIORITY FILING DATE: 2003-11-26  
PRIORITY APPLICATION NUMBER: 60/429,739  
PRIORITY FILING DATE: 2002-11-26  
NUMBER OF SEQ ID NOS: 8393  
SOFTWARE: PatentIn version 3.2  
; ID NO 7602  
; LENGTH: 1202  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
NAME/KEY: misc feature  
LOCATION: (271)..(271)  
OTHER INFORMATION: n is a, c, g, or t  
-723-860-7602

100% Match 93.1%; Score 512.8; DB 9; Length 1202;  
; Local Similarity 94.8%; Pred. No. 2e-141;  
; Cons 514; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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1  CTGGTGTGATGCGCATGATGCTGGAAGAAAGTCCGGCCGAGACACAGTTCCGGAAGC 60
202  CTGGTGTGATGCGCATGATGCTGGAAGAAAGTCCGGCCGAGACACAGTTCCGGAAGC 261
61  ACAGCCAGATGCGAGGATGCGGGAAGACCGCTCATGATGCTGCTGCGGCGACGCT 120
262  NNNNNNAGGATGCGAGGATGCGGGAAGACCGCTCATGATGCTGCTGCGGCGACGCT 321
121  CAGGGCTGCTCACTGCGCGGCTCTACAGATGCGCCAAAGCTTTGAACTGGAACCCCGAC 180
322  CAGGGCTGCTCACTGCGCGGCTCTACAGATGCGCCAAAGCTTTGAACTGGAACCCCGAC 381
181  AATGTGACCTTCTGTGCTGCTGCGGCTGCGGATGGAAGAGACGAGGCGCATCGCGCTGAC 240
382  AATGTGACCTTCTGTGCTGCTGCGGCTGCGGATGGAAGAGACGAGGCGCATCGCGCTGAC 441
241  ATTCATTTTAACTGATTCAGAGGCTTTCTGCTGCGAAGACATGCAATGATGCGGCTG 300
442  ATTCATTTTAACTGATTCAGAGGCTTTCTGCTGCGAAGACATGCAATGATGCGGCTG 501
301  GGGGATGTGCAAGCGGCTGCGGCTATGCTGCGGCGCGGCGAAGAGGCGGCTGCGCGGCG 360
502  GGGGATGTGCAAGCGGCTGCGGCTATGCTGCGGCGCGGCGAAGAGGCGGCTGCGCGGCG 561
361  GACCTGCACTGCACTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGAGATCCCGCTTG 420
562  GACCTGCACTGCACTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGAGATCCCGCTTG 621
421  GAGAAGCTGACCTGTTTTCGAGAGAGCGCGCATTAAGCATGAGTGGTCCAGATC 480
622  GAGAAGCTGACCTGTTTTCGAGAGAGCGCGCATTAAGCATGAGTGGTCCAGATC 681
481  ACCCTGCGGAGTGAAGAGCGCGGCGGAGACCTTGTGATGCACTGAGTGAAGCGCGCG 540
682  ACCCTGCGGAGTGAAGAGCGCGGCGGAGACCTTGTGATGCACTGAGTGAAGCGCGCG 741
541  GG 542
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Db 742 GG 743  
RESULT 15  
US-10-087-192-1355  
; Sequence 1355, Application US/10087192  
; Publication No. US20020182586A1  
GENERAL INFORMATION:  
APPLICANT: Morris, David W.  
APPLICANT: Engelhard, Eric K.  
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
TITLE OF INVENTION: CANCER  
FILE REFERENCE: 52945200012  
CURRENT APPLICATION NUMBER: US/10/087,192  
PRIORITY FILING DATE: 2002-03-01  
PRIORITY APPLICATION NUMBER: US 09/747,377  
PRIORITY FILING DATE: 2000-12-22  
PRIORITY APPLICATION NUMBER: US 09/798,586  
PRIORITY FILING DATE: 2001-03-02  
NUMBER OF SEQ ID NOS: 2059  
SOFTWARE: FaSTSeq for Windows Version 4.0  
; SEQ ID NO 1355  
; LENGTH: 1302  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-087-192-1355

Query Match 86.6%; Score 477; DB 6; Length 1302;  
Best Local Similarity 100.0%; Pred. No. 8e-131;  
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 66  CAGGATGCGAGGATGCGGGAAGCGCTGATGATGCTGCTGCGGCGAGCGTCAGGG 125
Db 397  CAGGATGCGAGGATGCGGGAAGCGCTGATGATGCTGCTGCGGCGAGCGTCAGGG 456
QY 126  CTGCTCACTGCGCGGCTCTACAGATGCGCCAAAGCTTTGAACTGGAACCCCGACATGT 185
Db 457  CTGCTCACTGCGCGGCTCTACAGATGCGCCAAAGCTTTGAACTGGAACCCCGACATGT 516
QY 186  GACCTTCTGTGCTGCTGCGGCTGCGGATGGAAGAGACGAGGCGCATCGCGCTGACATCA 245
Db 517  GACCTTCTGTGCTGCTGCGGCTGCGGATGGAAGAGACGAGGCGCATCGCGCTGACATCA 576
QY 246  TTTTACGCTGATTCAGAGGCTTTCTGCTGCGAAGACATGCAATGATGCGGCTGAGCGA 305
Db 577  TTTTACGCTGATTCAGAGGCTTTCTGCTGCGAAGACATGCAATGATGCGGCTGAGCGA 636
QY 306  TGTGACGCGGCTGCGGCTATGCTGCGGCGCGCGAGAGAGCGGCTGCGCGGCGACCT 365
Db 637  TGTGACGCGGCTGCGGCTATGCTGCGGCGCGCGAGAGAGCGGCTGCGCGGCGACCT 696
QY 366  GCACTGCACTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGAGATCCCGCTTGAAGAA 425
Db 697  GCACTGCACTCTCATTTTGAACCCCAAGAGAGCGCTGGAAGAGATCCCGCTTGAAGAA 756
QY 426  GCTGACCTGTTTTCGAGAGAGCGCGCATTAAGCATGAGTGGTCCAGATCACCCT 485
Db 757  GCTGACCTGTTTTCGAGAGAGCGCGCATTAAGCATGAGTGGTCCAGATCACCCT 816
QY 486  CCCCAGTGAAGAGCGCGGCGGAGACCTTGTGATGCACTGAGTGAAGCGCGCGG 542
Db 817  CCCCAGTGAAGAGCGCGGCGGAGACCTTGTGATGCACTGAGTGAAGCGCGCGG 873
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Search completed: June 4, 2006, 22:46:17  
Job time : 1112 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd

nucleic - nucleic search, using sw model

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on:      June 4, 2006, 22:29:22 ; Search time 25 Seconds
        (without alignments)
        2595.739 Million cell updates/sec
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a:      US-10-089-641-1
act score: 551
ance:    1 ctgcttgatcgacattatgac.....acgccccggggccttagagc 551

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table: IDENTITY_NUC
      100

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Gapor 10.0 , Gapext 1.0

ched: 246837 seqs, 58886990 residues

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.. number of hits satisfying chosen parameters: 493674
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:um DB seq length: 0
:um DB seq length: 20000000000

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..processing: Minimum Match 0%
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Listing first 45 summaries

base :

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2: /BMC_Celerra_S10S3/ptocdata/2/pubpna/US06_NEW_PUB_seq.*
3: /BMC_Celerra_S10S3/ptocdata/2/pubpna/US07_NEW_PUB_seq.*
4: /BMC_Celerra_S10S3/ptocdata/2/pubpna/US08_NEW_PUB_seq.*
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7: /BMC_Celerra_S10S3/ptocdata/2/pubpna/US11_NEW_PUB_seq.*
8: /BMC_Celerra_S10S3/ptocdata/2/pubpna/US60_NEW_PUB_seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

t	Score	Query Match	Length	DB	ID	Description
1	405.8	73.6	574	6	US-10-888-619-1846	Sequence 1846, App
2	154.4	28.0	1343	7	US-11-297-160-1	Sequence 1, Appli
3	154.4	28.0	1355	6	US-10-505-928-798	Sequence 798, App
4	110.8	20.1	609	6	US-10-888-619-1845	Sequence 1845, App
5	51	9.3	979	6	US-10-953-349-36159	Sequence 36159, A
6	41.8	7.6	1292	6	US-10-953-349-33740	Sequence 32740, A
7	41.4	7.5	813	7	US-11-255-290-11	Sequence 11, Appli
8	40.4	7.3	813	6	US-10-953-349-30766	Sequence 30766, A
9	40.2	7.3	1837	6	US-10-953-349-33182	Sequence 35182, A
10	40	7.3	1582	6	US-10-953-349-35342	Sequence 35342, A
11	39.4	7.2	1252	6	US-10-925-647-29	Sequence 29, Appl
12	39.2	7.1	1815	6	US-10-953-349-28360	Sequence 28360, App
13	38.8	7.0	1188	6	US-10-953-349-28881	Sequence 28881, A
14	38.4	7.0	832	6	US-10-953-349-34511	Sequence 34511, A
15	38.2	6.9	1122	6	US-10-953-349-31614	Sequence 31614, A
16	38	6.9	2697	6	US-10-953-349-35363	Sequence 35363, A
17	37.8	6.9	833	6	US-10-953-349-22595	Sequence 26595, A
18	37.4	6.8	1487	6	US-10-888-619-1846	Sequence 1846, App
19	37.2	6.8	1487	6	US-10-953-349-31193	Sequence 31193, A
20	37.2	6.8	1929	7	US-11-334-622-1	Sequence 1, Appli
21	37.2	6.8	1929	7	US-11-334-622-5	Sequence 5, Appli
22	37.2	6.8	1959	7	US-11-334-622-3	Sequence 3, Appli
23	37.2	6.8	1971	7	US-11-334-622-7	Sequence 7, Appli
24	37	6.7	1473	7	US-10-953-349-36062	Sequence 36062, A
25	36.8	6.7	778	6	US-10-953-349-30106	Sequence 30106, A

45	35	6.4	2912	6	US-10-50S-928-685	Sequence 685, App
44	35	6.4	1723	6	US-10-95S-349-77999	Sequence 72999, A
43	35	6.4	1501	6	US-10-95S-349-92223	Sequence 32223, A
42	35	6.4	1038	6	US-10-95S-349-82820	Sequence 28202, App
41	35.2	6.4	2104	7	US-11-29S-697-1240	Sequence 1240, App
40	35.2	6.4	2043	6	US-10-95S-349-11315	Sequence 11315, A
39	35.2	6.4	1924	6	US-10-95S-349-4671	Sequence 34671, A
38	35.2	6.4	1114	6	US-10-95S-349-92119	Sequence 32119, A
37	35.4	6.4	1913	7	US-11-312-958-811	Sequence 41, Appl
36	35.4	6.4	1689	6	US-10-95S-349-94571	Sequence 4571, A
35	35.6	6.4	1050	6	US-10-95S-349-91244	Sequence 31244, A
34	35.6	6.4	1255	6	US-10-95S-349-35480	Sequence 35480, A
33	35.6	6.5	979	6	US-10-95S-349-44412	Sequence 34412, A
32	35.8	6.5	2916	7	US-11-29S-697-775	Sequence 775, App
31	35.8	6.5	916	6	US-10-95S-349-94694	Sequence 34694, A
30	35.8	6.5	813	6	US-10-95S-349-95371	Sequence 25371, A
29	36	6.5	1214	6	US-10-95S-349-97211	Sequence 27211, A
28	36.2	6.6	1818	6	US-10-95S-349-92720	Sequence 32720, A
27	36.6	6.6	1338	6	US-10-95S-349-92488	Sequence 32488, A
26	36.6	6.6	1017	6	US-10-95S-349-88608	Sequence 28608, A

## ALIGNMENTS

```

RESULT 1
US-10-488-619-1846
: Sequence 1846, Application US/10486619
: Publication No. US20060092578A1
:
GENERAL INFORMATION:
: APPLICANT: Greentlee, Winner and Sullivan, P.C.
: TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
: FILE REFERENCE: 98-01 WO
: CURRENT APPLICATION NUMBER: US/10/488,619
: NUMBER OF SEQ ID NOS: 3040
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 1846
: LENGTH: 574
:
TYPE: DNA
: ORGANISM: Mus musculus
: US-10-488-619-1846

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Query Match	73.68;	Score 405.8;	DB 6;	Length 574;
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Best Local Similarity 87.7%; Pred. No. 2.3e-85;

Matches	443;	Conservative	0;	Mismatches	62;	Indels	0;	Gaps	0.
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[illegible]

430 ACCGTGATGACATCCATCTTGAATCCATGATGACATGAGGAGCCCTGCTTGG 489  
 422 AGAAGCTCAGCCTGTTTTCGAGAGAGCGCAGCCTTAAGCACTGGTCCAGCATCA 481  
 490 AGAAGCTCAGTGTGTTCTGCGAGAGAGCGCAGCCTTAAGCACTGGTCCAGCATCA 549  
 482 CCCCTCCCGAGTGACAGCCCGGCGG 506  
 550 CCCCTCCCGAGTGACAGCCCTGGCAG 574

T 2  
 -297-160-1  
 uence 1, Application US/11297160  
 ublication No. US2006008888A1  
 ERAL INFORMATION:  
 PLICANT: Wang, Xin Wei  
 PLICANT: Harris, Curtis C.  
 PLICANT: Fornace Jr., Albert J.  
 PLICANT: Courseen, Jill D.  
 PLICANT: Zhan, Qimin  
 PLICANT: The Government of the United States of America  
 PLICANT: as represented by the Secretary of the  
 PLICANT: Department of Health and Human Services  
 TLE OF INVENTION: Methods for Identifying Inhibitors of GADD45  
 TLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity  
 LE REFERENCE: 015280-367100US  
 RRENT FILING DATE: 2005-12-07  
 RRENT APPLICATION NUMBER: US/11/297,160  
 R FILING DATE: 2003-06-20  
 R APPLICATION NUMBER: US/09/534,811  
 R FILING DATE: 2000-03-24  
 R APPLICATION NUMBER: US 60/126,069  
 R FILING DATE: 1999-03-25  
 R OF SEQ ID NOS: 32  
 FTWARE: PatentIn Ver. 2.1  
 ID NO 1  
 LENGTH: 1343  
 YPE: DNA  
 GANISM: Homo sapiens  
 NATURE:  
 NAME/KEY: CDS  
 CATION: (284)..(781)  
 HER INFORMATION: human growth arrest and DNA-damage-inducible  
 HER INFORMATION: protein (GADD45)  
 -297-160-1

ry Match 28.0%; Score 154.4; DB 7; Length 1343;  
 e Local Similarity 61.0%; Pred. No. 1.6e-27;  
 ches 282; Conservative 0; Mismatches 156; Indels 24; Gaps 1;  
 54 GGAAGACACAGCAGATGAGGATGCGGGAAGCGCTCATGATGTTGCTGTCGCG 113  
 313 GCAGAAAGCCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 372  
 114 GCAGCGTCAAGGCTGCTCACTGCGGCGCTTACGATCAGCCAAAGCTTTGAACGTGA 173  
 373 CTGAGTCAAGCGACATCACTGTCGGGGGTGTACGAAGCGGCAAGCTCTCAACGTCGA 432  
 174 CCCCCGCAATGATACCTTCTGTGTGCTGCGGTGAGAGAGAGAGAGAGAGAGAGAG 233  
 433 CCCCCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 492  
 234 GTCGAGATCCATTTTACGTCGATCCAGGCTTTCTGCTGCGAAGACGATCCAGATAGT 293  
 493 TCTGCAATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 552  
 294 GCGCGTGGGCGATGTCAGCGGCTGCGGCTTATCGTG----- 330  
 553 GCGCGTCAAGCAACCGGCGCGGCTGCGGCGGAGCTCTGCTTGGAGACCGACGCTGGCC 612

Qy 331 -GGCGCCGCGAGAGAGCGGCGGTCGCCCGGCGACCTGCATGATCTCTTTCGAAACC 389  
 Db 613 CGCGGAGCGAGGCGGCGGCGAGAGCGCGGAGCTGACCTGCTGCTGTGATGACGAATCC 672  
 Qy 390 CAACGAGAGCGCTGGAAGATCCCGCTTGGAGAGACTCAGCTGTTTTCGAGAGAG 449  
 Db 673 ACATTTCATCAATGGAAGATCTGCTTAAGTCAACTTATTTGTTTTCGCGGGAAG 732  
 Qy 450 CCGCAGCGTTAACGACTGGGTGCCAGCATCACTTCCCGCA 491  
 Db 733 TCGCTACATGATCAATGGGTTCAGATTAATCTTCCCTGA 774

RESULT 3  
 US-10-505-928-798  
 ; Sequence 798, Application US/10505928  
 ; Publication No. US20060088532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
 ; FILE REFERENCE: 28967/39178  
 ; CURRENT APPLICATION NUMBER: US/10/505,928  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/363,019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; NUMBER OF SEQ ID NOS: 866  
 ; SOFTWARE: PatentIn 3.2  
 ; SEQ ID NO 798  
 ; LENGTH: 1355  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-505-928-798

Query Match 28.0%; Score 154.4; DB 6; Length 1355;  
 Best Local Similarity 61.0%; Pred. No. 1.6e-27;  
 Matches 282; Conservative 0; Mismatches 156; Indels 24; Gaps 1;  
 Qy 54 GGAAGACACAGCAGATGAGGATGCGGGAAGCGCTCATGATGTTGCTGTCGCG 113  
 Db 325 GCAGAAAGCCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 384  
 Qy 114 GCAGCGTCAAGGCTGCTCACTGCGGCGCTTACGATCAGCCAAAGCTTTGAACGTGA 173  
 Db 385 CTGAGTCAAGCGACATCACTGTCGGGGGTGTACGAAGCGGCAAGCTCTCAACGTCGA 444  
 Qy 174 CCCCCGCAATGATACCTTCTGTGTGCTGCGGTGAGAGAGAGAGAGAGAGAGAGAG 233  
 Db 445 CCCCCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 504  
 Qy 234 GCTGAGATCCATTTTACGTCGATCCAGGCTTTCTGCTGAGAAAGCATGACATAGT 293  
 Db 505 TCTGCAATCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACT 564  
 Qy 294 GCGCGTGGGCGATGTCAGCGGCTGCGGCTTATCGTG----- 330  
 Db 565 GCGCGTCAAGCAACCGGCGCGGCTGCGGAGCTCTGCTTGGAGACCGACGCTGGCC 624  
 Qy 331 -GGCGCCGCGAGAGAGCGGAGTCCCGGCGACCTGCACTGATCTTTCGAACC 389  
 Db 625 CCGGCGAG 684  
 Qy 390 CAACGAGAGCGCTGGAAGATCCCGCTTGGAGAGACTCAGCTGTTTTCGAGAGAG 449  
 Db 685 ACATTTCATCAATGGAAGATCTGCTTAAGTCAACTTATTTGTTTTCGCGGGAAG 744  
 Qy 450 CCGCAGCGTTAACGACTGGGTGCCAGCATCACTTCCCGCA 491  
 Db 745 TCGCTACATGATCAATGGGTTCAGATTAATCTTCCCTGA 786

RESULT 4  
 US-10-488-619-1845/c  
 ; Sequence 1845, Application US/10488619



PRESENT FILING DATE: 2005-10-20  
 APPLICATION NUMBER: 60/620,896  
 FILING DATE: 2004-10-21  
 APPLICATION NUMBER: 60/646,728  
 FILING DATE: 2005-01-24  
 APPLICATION NUMBER: 60/673,925  
 FILING DATE: 2005-04-22  
 OF SEQ ID NOS: 11  
 PATENT: PatentIn version 3.2  
 ID NO: 11  
 LENGTH: 813  
 TYPE: DNA  
 ORGANISM: unknown  
 NAME: Thermus thermophilus endonuclease IV  
 -255-290-11

	7.5%;	Score 41.4;	DB 7;	Length 813;
Local Similarity	44.8%;	Pred. No. 0.13;		
Conservative	0;	Mismatches 196;	Indels 0;	Gaps 0;

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97 GAGTGTCTGCTGTTCGGCGCAGCGCTCAAGGGTGCTCACTGCCGCGCTTACAGATGAGCC 156
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235 GAGGGGAGGCTTTGGGGAAGAAGCGTGCAGGCTTGCGCAGCATCGAAGAGGCGCGC 294
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
157 AAGTCTTGAACGTGACCCCGACAATGTGACTTCTGTGTGTGCTCGCTCGGGTAGAG 216
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
295 CTCTCGGGGTGAAGTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 354
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217 GACGAGGGCGACATCGCGCTGCAGATTCATTATTAAGCTGATCCAGGCTTTCTGCTCGAG 276
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355 GAAGGGGCGCTCAAGGCGCTGTGCGCTGTGCGCGCGGTGCGCTGCCGCGCTCTCTGTG 414
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
277 AACGACATCGACATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 336
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
415 GAGAACCGCCCCGGGGCGGGAGAAAGTGGGGCGCGGTTTGAAGAGCTGTGGCTG 474
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
337 GGGGAGGAGGGGGGTGGCGCGGGCGACCTGCACTGCATCTTCATTTCGAACCACAAGAG 396
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
475 GTGGCGGACACCCCCCTTCAGAGTGTGCTGTGAACACTGCGCACCTTAACCGCGGGTAC 534
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
397 GACGCCGTGAAGATCCCGCCTTGGAGAACCTGAGCTGTTTTTGGAGAGAGCC 451
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
535 GACGTGCGCAGAGACCCCTTGGGGGTCTGTGAAGCGCTGTGACGGGCGGTGGGCC 589
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T 8  
 1-953-349-30766  
 Sequence 30766, Application US/10953349  
 Publication No. US20060107345A1  
 SERIAL INFORMATION:  
 APPLICANT: ALEXANDROV, Nickolai et al.  
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 FILE OR INVENTION: ENCODED THEREBY  
 LE REFERENCE: 2750-1579PUS2  
 PRESENT APPLICATION NUMBER: US/10/953,349  
 PRESENT FILING DATE: 2004-09-30  
 MEMBER OF SEQ ID NOS: 40252  
 SOFTWARE: PatentIn version 3.3  
 ID NO: 30766  
 LENGTH: 813  
 TYPE: DNA  
 ORGANISM: Triflicum aestivum  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (214)..(214)  
 OTHER INFORMATION: n is a, c, g, or t  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (217)..(217)  
 OTHER INFORMATION: n is a, c, g, or t  
 -953-349-30766

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Query Match      7.3%; Score 40.4; DB 6; Length 813;
Best Local Similarity 47.8%; Pred. No. 0.23;
Matches 115; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 213 GAGAGACGAGGCGCAGCATCCGCGCTGCAGATCCATTTCAGCTGATCCAGGCTTTTGCTG 272
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Db 455 GGGGAGACGAGGAGGCGCCCTCGGCGCGTACGCGGAGAGAGCGGCGGCTCGGCGGCGGAG 514

QY 273 CGAGAACGACATCGACATPAGTGGCGCGTGGCGGATGTGTGACGCGGCTGGCGGCTATGTAGG 332
   |||
Db 515 GGCCTCGGCGCGTGGCGGCTGTGTGGGCTGTGACTCTCGGCGCTTCGACAGAGCGGCGGCTGG 574

QY 333 CGCGCGGAGAGGCGGCGGTGCGCCGCGGCGACTTGCACTGCATCTTCATTTCGAACCCCA 392
   |||
Db 575 CGCGCGGTGGAGGCGGCGGCTGGCGCGCTGCTTCGGCGCACGCGCGGCTCGACGCGCTGTCA 634

QY 393 CGAGGAGCGCTCGAAGGATCCGCGCTTGGAGAGTCGACCTGTTTTCGAGAGAGCGCG 452
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Db 635 CTGCTGTCTTCACGAGGAGGAGTGCACAGACTGCTTCAGCGTACTGAAGATGAGTACAA 694

QY 453 CA 454
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Db 695 CA 696

RESULT 9
US-10-953-349-35182
; Sequence 35182, Application US/10953349
; Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DERIVED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCODED THERAPEUTIC
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35182
LENGTH: 1837
TYPE: DNA
ORGANISM: Zea mays subsp. mays
US-10-953-349-35182

Query Match      7.3%; Score 40.2; DB 6; Length 1837;
Best Local Similarity 47.8%; Pred. No. 0.29;
Matches 117; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 77 GTGCGCGGAAAGCGCTGCATGATGTGCTGTGTGCGCGCAGCGTGCAGGCGTGCCTCACTG 136
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Db 228 GGGGAGTGGCATTCGCTGCGCGGCGGAGGCTTCGAGGCAAGCGGTGGCGGCTTCGACGG 287

QY 137 CCGGCGTCTACGAGTCAAGCTTCTGAACGTGAGACCCGACACATGTGACTTCTGTG 196
   |||
Db 288 CCGGCGGCGCGCCCGGCGCGCCGCGTGGCGGAGAGGCGGCGGCTTGTGGCGCTGTGACT 347

QY 197 TGTGCGCTGCGGAGTGAAGAGACGAGCGGCGACATGCGCGCTGCAGATTCATTTCAGCTGA 256
   |||
Db 348 ACGAGGCGCTTGGCGGCTGAGCTGTGAGGCGCGCTCGCCCTGAGATTCATGATTCGGGCGC 407

QY 257 TCCAGGCTTCTGTGTCGAGAACGACATGACATAGTGCCTGGCGGAGTGTGACGCGCG 316
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Db 408 TGGCCATGTTGGCTCCGAATTCGCATTCGCTTCAGCGGCGCGGAGGAGCTGTGGCGCTGA 467

QY 317 TGGCG 321
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Db 468 TCGAG 472

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HERAL INFORMATION:  
 APPLICANT: ALEXANDROV, Nikolai et al.  
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 TITLE OF INVENTION: ENCONDED THERBY  
 FILE REFERENCE: 2750-1579PUS2  
 CURRENT APPLICATION NUMBER: US/10/953,349  
 NUMBER OF SEQ ID NOS: 40252  
 SOFTWARE: PatentIn version 3.3  
 LENGTH: 1582  
 TYPE: DNA  
 ORGANISM: Zea mays subsp. mays  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (468)..(469)  
 OTHER INFORMATION: n is a, c, g, or t  
 0-953-349-35342

7.3%; Score 40; DB 6; Length 1582;  
 Local Similarity 47.9%; Pred. No. 0.32;  
 Mismatches 125; Indels 0; Gaps 0;

251 CGCTGATCCAGGCTTTTCTGCTGCGAAGAACATCGCATAGTCCGCTGGCGATGTC 310  
 694 CGCTCCCTCTACTCGGCTCTGCGACCGCATGAGTCTGCGCTGCGCTGACCTCA 753  
 311 AGGGGCGGGGGGCTATCGTGGGCGCGGAGAGGCGGGTGGCGGACCTTGACT 370  
 754 GGTGCTCGATCCATCGCGCGCCACAGACGCGCTCAAGCGCTGAGAGAAAGGCGT 813  
 371 GCATCTCATTTTCGAAACCCCAACGAGACGCTTGAAGATCCCGCTTGAGAACTCA 430  
 814 GCATCGCTACTCTCGCTCGCGCGACGCGCTCAAGCGCTGAGAGAAAGGCGT 873  
 431 GCGTCTTTTGGAGAGAACCGCGACGCTTAAACAGCTGGTGTCCAGCATATCCTCCCG 490  
 874 CGCATTTCTTCAGGCGGCTCTCTGCTCGCGCGCGCTCTCTGTGGAACGCGCTCACG 933

0-525-647-29  
 Sequence 29, Application US/10525647  
 Publication No. US20060112442A1  
 HERAL INFORMATION:  
 APPLICANT: CropDesign N.V.  
 TITLE OF INVENTION: Rice promoters  
 FILE REFERENCE: CD-071-PCT  
 CURRENT APPLICATION NUMBER: US/10/525,647  
 CURRENT FILING DATE: 2005-02-24  
 PRIOR APPLICATION NUMBER: EP 03075331.3  
 RIOR FILING DATE: 2003-02-04  
 NUMBER OF SEQ ID NOS: 88  
 SOFTWARE: PatentIn version 3.1  
 LENGTH: 1252  
 TYPE: DNA  
 ORGANISM: Oryza sativa  
 FEATURE:  
 NAME/KEY: misc feature  
 OTHER INFORMATION: TC89891 (PRO0081)  
 NAME/KEY: misc feature  
 LOCATION: (5)..(5)  
 OTHER INFORMATION: n = any nucleotide  
 0-525-647-29

7.2%; Score 39.4; DB 6; Length 1252;  
 Local Similarity 45.2%; Pred. No. 0.42;  
 Mismatches 176; Indels 0; Gaps 0;

169 GTGAGCCCGCATGTGACCTTCTGTGCTGCGCTGGGGTGAGAGAGAGGCGGAC 228

Db 511 GAGAACTGAGACGAGTCTCGCCGAGAGAGCGCGCGCGGCGGCGGCTTCAC 570  
 Qy 229 ATGCGCTGAGATCATTTTACGCTGATCCAGGCTTTTCTGCTCGAAGACATCGAC 288  
 Db 571 TTGCGCTGCTGAGACCGGACGAGCCAACTACGTCAAGTACACAGACGCTGCGAG 630  
 Qy 289 ATAGTCCGGGTGGGCGCATGTGACGAGCGGCTGGCGGCTTATCGTGGCGCGGAGAGCG 348  
 Db 631 CTGCTGCGGTGCGCGGCGGACATCGTGTACGACACGCTGTGGCGCGGACGCTGCGG 690  
 Qy 349 GGTGCGCGGCGGACCTGACATCGATCTCATTTTGAACCCCAAGAGAGCGCTTGAAG 408  
 Db 691 CTGCGCGCGGACACGCGGCTGCTGAGACCGAGAGTTCTCCGTGCGCATAGGAG 750  
 Qy 409 GATCCGCTTGGAGAAAGCTCAGCTGTTTGGAGAGAGCGGACGCTTAACGACTGG 468  
 Db 751 CTCACCTCCAGGCTCGCGCGGACCGCGCATGAGGTCGACGCTGCGCATGCGGAC 810  
 Qy 469 GTGCCAGCATCACCTCCGCC 489  
 Db 811 GGCATCACCATCTGCGCGCGC 831

RESULT 12  
 US-10-953-349-28360/C  
 Sequence 28360, Application US/10953349  
 Publication No. US20060107345A1  
 GENERAL INFORMATION:  
 APPLICANT: ALEXANDROV, Nikolai et al.  
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 TITLE OF INVENTION: ENCONDED THERBY  
 FILE REFERENCE: 2750-1579PUS2  
 CURRENT APPLICATION NUMBER: US/10/953,349  
 CURRENT FILING DATE: 2004-09-30  
 NUMBER OF SEQ ID NOS: 40252  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 28360  
 LENGTH: 1815  
 TYPE: DNA  
 ORGANISM: Triticum aestivum  
 US-10-953-349-28360

Query Match 7.1%; Score 39.2; DB 6; Length 1815;  
 Best Local Similarity 51.7%; Pred. No. 0.5; Mismatches 83; Indels 0; Gaps 0;

Matches 89; Conservative 0; Mismatches 83; Indels 0; Gaps 0;  
 Qy 90 GTCGATGAGTGTGCTGCTGCGGCGACGCTGAGGCGTCTCACTGCGGCGTCTACGA 149  
 Db 1708 GCACTGGAACAGACCTGAGAGGAGCGGCTCTCCCTGCGCGCGTCAAGAGCCCT 1649  
 Qy 150 GTCAGCCAAAGTCTTGAACGTGACCCGACATGTACCTTCTGTGCTGCTGCGG 209  
 Db 1648 CGCGCGGAGCGCTCCAAAGCGGACCTCTCGAGGTGACAGGAGAACTTGTGTGCGAT 1589  
 Qy 210 TGAGAGAGAGAGGCGCATCGGCTGACGATCATTTTACGCTGATTCAG 261  
 Db 1588 TAAGATGACAGAGAGAGGCTTCTGCAATTGAGCGTTTGAAGCTTAAGTAAG 1537

RESULT 13  
 US-10-953-349-28881/C  
 Sequence 28881, Application US/10953349  
 Publication No. US20060107345A1  
 GENERAL INFORMATION:  
 APPLICANT: ALEXANDROV, Nikolai et al.  
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 TITLE OF INVENTION: ENCONDED THERBY  
 FILE REFERENCE: 2750-1579PUS2  
 CURRENT APPLICATION NUMBER: US/10/953,349  
 CURRENT FILING DATE: 2004-09-30  
 NUMBER OF SEQ ID NOS: 40252  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 28881

LENGTH: 1188  
TYPE: DNA  
ORGANISM: Triticum aestivum  
1-953-349-28881

Query Match 7.0%; Score 38.8; DB 6; Length 1188;  
Local Similarity 56.2%; Pred. No. 0.57; Indels 0; Gaps 0;  
Ches 73; Conservative 0; Mismatches 57;

294 GCGCGGCGGATGTGACGCGGCTGCTATCTGTCGCGCGCGGAGAGCGGATGC 353  
237 GCTTCGCGCGCGCGGAGCCATTAAGCGGCGATGTGGGACAGCGCTTGAGGGCTCAC 178  
354 GCGGCGCGACCTGCACTGATCTCTCAATTTGAAACCCCAAGAGAGCGCTGGAAGATCC 413  
177 GGTGGGAGACGCCCAACCGAGAGAGGAGCGGCGCGGAGAGGCGGCGACAGCGGACA 118  
414 CGCCTTGAG 423  
117 CGACGTCGAG 108

T 14  
1-953-349-34511  
Sequence 34511, Application US/10953349  
Publication No. US20060107345A1  
INVENTOR: ALEXANDROV, Nikolai et al.  
INVENTOR INFORMATION:  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
TITLE OF INVENTION: ENCODED THEREBY  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
ID NO 34511  
LENGTH: 832  
TYPE: DNA  
ORGANISM: Zea mays subsp. mays  
1-953-349-34511

Query Match 7.0%; Score 38.4; DB 6; Length 832;  
Local Similarity 45.8%; Pred. No. 0.66; Indels 0; Gaps 0;  
Ches 132; Conservative 0; Mismatches 156;

184 GTGACCTTCTGTGTGCTGCTGCGGTGAGAGAGAGCGGCGACATCGCTGCAGATC 243  
189 GCGACCTGCGGATC 248  
244 CATTTACGCTGATCCAGGCTTTCTGTGCGAAGACGATGACATATGCGCGTGGGC 303  
249 ACCAG 308  
304 GATGTGACAG 363  
309 GCGCGGCTGAGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368  
364 CTGCACTGATCTCTCAATTTGAAACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 423  
369 ATCAAGTCATCTTTCATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 428  
424 AAGCTGAGCTGTTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471  
429 TACCTCAAGGCGCGAG 476

T 15  
1-953-349-31614  
Sequence 31614, Application US/10953349  
Publication No. US20060107345A1  
INVENTOR: ALEXANDROV, Nikolai et al.  
INVENTOR INFORMATION:  
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCODED THEREBY  
FILE REFERENCE: 2750-1579PUS2  
CURRENT APPLICATION NUMBER: US/10/953,349  
CURRENT FILING DATE: 2004-09-30  
NUMBER OF SEQ ID NOS: 40252  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 31614  
LENGTH: 1122  
TYPE: DNA  
ORGANISM: Triticum aestivum  
US-10-953-349-31614

Query Match 6.9%; Score 38.2; DB 6; Length 1122;  
Best Local Similarity 59.8%; Pred. No. 0.77; Indels 43; Gaps 0;  
Matches 64; Conservative 0; Mismatches 43;

QY 295 CCGGTGCGGATGTGACGCGGCTGCTATCTGTCGCGCGCGGAGAGAGCGGATGC 354  
Db 234 CGTGGCGGCGGTGGAAGGAGAGGCGCGGATGGAAGGAGGAGAGAGAGAGAGAG 293  
QY 355 CCGGCGGACCTGCACTGATCTCTCAATTTGAAACCCCAAGAGAGAGAGAGAG 401  
Db 294 CCGCAAG 340

Search completed: June 4, 2006, 22:46:47  
Job time : 25 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

Protein - protein search, using sw model

on: June 2, 2006, 22:32:40 ; Search time 86 Seconds  
(without alignments)  
845.319 Million cell updates/sec

US-10-089-641-2  
1 MTLREVRGQDTPVETSTARMQ.....LFCESRSVNDVPSITLPE 159

ing table: BLOSUM62

hed: 2589679 seqs, 457216429 residues

number of hits satisfying chosen parameters: 2589679

um DB seq length: 0  
um DB seq length: 200000000

rocessing: Minimum Match 0%

Listing first 45 summaries

ase :  
1: A\_Geneseq\_8:\*  
2: geneseqp1980s:\*  
3: geneseqp1990s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

lt	Score	Match	Length	ID	Description
1	826	100.0	159	2 AAW08138	Aaw08138 Human cyt
2	826	100.0	159	2 AAY87957	Aay87957 Human CR6
3	826	100.0	159	6 ABR40340	AbR40340 Human CR6
4	826	100.0	159	7 ADG62828	AdG62828 Human gro
5	826	100.0	159	7 ADP65201	AdP65201 Human gro
6	826	100.0	159	8 ADJ75308	AdJ75308 Marker ge
7	826	100.0	159	8 ADX85166	AdX85166 Human gad
8	826	100.0	159	9 AED74299	Aed74299 Human pla
9	811	98.2	160	3 AAB13772	Aab13772 Human SYG
10	804	97.3	159	2 AAW23533	Aaw23533 Human GRP
11	787	95.3	159	6 ABR40341	AbR40341 Mouse gad
12	787	95.3	159	8 ADJ76135	AdJ76135 Marker ge
13	787	95.3	159	8 ADX85168	AdX85168 Mouse gad
14	737	89.2	141	7 AAW85647	Aaw85647 Human pro
15	728	88.1	185	9 ADV77059	Adv77059 Huntingto
16	710	86.0	158	7 AAW85646	Aaw85646 Mouse pro
17	550	66.6	104	3 AAB34425	Aab34425 Human sec
18	550	66.6	104	3 AAB34424	Aab34424 Gene 41 h
19	457.5	55.4	165	2 AAR53669	Aar53669 Sequence
20	457.5	55.4	165	6 ABU07405	AbU07405 Protein d
21	457.5	55.4	165	6 ABR40338	AbR40338 Human gad
22	457.5	55.4	165	7 ADE57334	AdE57334 Human pro
23	457.5	55.4	165	7 ADE57322	AdE57322 Human pro

24	457.5	55.4	165	7 ADE60790	AdE60790 Human pro
25	457.5	55.4	165	7 ADE60786	AdE60786 Human pro
26	457.5	55.4	165	7 ADE57330	AdE57330 Human pro
27	457.5	55.4	165	7 ADE60778	AdE60778 Human pro
28	457.5	55.4	165	7 ADE57326	AdE57326 Human pro
29	457.5	55.4	165	7 ADE60782	AdE60782 Human pro
30	457.5	55.4	165	7 AD045473	Ad045473 Human pro
31	457.5	55.4	165	7 ADG62823	AdG62823 Human gro
32	457.5	55.4	165	7 ADN95873	Adn95873 Human BRC
33	457.5	55.4	165	9 ADX85162	AdX85162 Human gad
34	457.5	55.4	165	9 ADX26281	AdX26281 Novel cel
35	457.5	55.4	165	9 ADY15163	AdY15163 PRO polyp
36	457.5	55.4	165	9 ADY20500	AdY20500 PRO polyp
37	457.5	55.4	165	9 AEB54702	Aeb54702 Human gro
38	457.5	55.4	165	9 AEC07458	Aec07458 Protein s
39	457.5	55.4	165	9 AED07116	Aed07116 Respirato
40	451.5	54.7	165	6 ABR40339	AbR40339 Mouse gad
41	451.5	54.7	165	6 ABR40337	AbR40337 Mouse gad
42	451.5	54.7	165	7 ADG62829	AdG62829 Mouse gro
43	451.5	54.7	165	9 ADX85164	AdX85164 Mouse gad
44	451.5	54.7	165	9 ADX26350	AdX26350 Novel cel
45	447	54.1	160	7 ADG62827	AdG62827 Human gro

## ALIGNMENTS

RESULT 1  
ID AAW08138 standard; protein; 159 AA.  
AC AAW08138;  
DT 11-MAR-1997 (first entry)  
DE Human cytokine response protein CR6.  
KW Cytokine response protein; CR6; interleukin-2; IL-2;  
KW ligand-stimulated gene expression; diagnosis; therapy.  
XX  
OS Homo sapiens.  
XX  
PN W096339427-A1.  
XX  
PD 12-DEC-1996.  
XX  
PF 05-JUN-1996; 96WO-US009194.  
XX  
PR 05-JUN-1995; 95US-00461379.  
PR 05-JUN-1995; 95US-00462337.  
PR 05-JUN-1995; 95US-00462390.  
PR 05-JUN-1995; 95US-00463074.  
PR 05-JUN-1995; 95US-00463081.  
PR 05-JUN-1995; 95US-00465585.  
XX  
PA (DART-) DARTMOUTH COLLEGE.  
XX  
XX Smith KA, Beadling C;  
XX WPI: 1997-043062/04.  
XX N-PSDB; AAT4381.  
XX  
XX Cytokine response proteins and genes - used in the detection and therapy  
XX of diseases caused by a mutation in the CR coding region.  
XX  
XX Claim 6; Page 29-30; 81pp; English.  
XX  
XX Cytokine response proteins CR1-CR8 (AAW08133-40) are encoded by genes  
XX (see also AAT43376-83) isolated from a chiol-selected interleukin-2-  
XX induced human T-cell blast cDNA library. 6 genes (CR1, 2, 3, 5, 6, 8) are  
XX novel. CR6 belongs to a family of small nuclear-localising gene products.  
XX It binds to p21 and may facilitate cellular proliferation by preventing  
XX the inhibitory activity of p21. Recombinant CR6 polypeptides can be

produced and used to identify inhibitors of DNA replication of use as anti-proliferative agents e.g. in the treatment of cancer

Sequence 159 AA;

ry Match 100.0%; Score 826; DB 2; Length 159;  
Local Similarity 100.0%; Pred. No. 3.7e-89; Indels 0; Gaps 0;  
ches 159; Conservative 0; Mismatches 0;

```
1 MTLSEVRGDDTVPESTARMOGAKALHELLLSAQRQGCCTAGYSAKYLVNDPNDVTRC 60
1 MTLSEVRGDDTVPESTARMOGAKALHELLLSAQRQGCCTAGYSAKYLVNDPNDVTRC 60
1 MTLSEVRGDDTVPESTARMOGAKALHELLLSAQRQGCCTAGYSAKYLVNDPNDVTRC 60
61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVQRLAIVAGGEAGAPGDLHCT 120
61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVQRLAIVAGGEAGAPGDLHCT 120
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
```

18-SEP-2000 (first entry)  
AA87957;  
AA87957 standard; protein; 159 AA.

Human CR6 protein.

CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment; cell differentiation; cancer; immune disease; rheumatologic disease; transplant rejection; anti-infective; CR6.

Homo sapiens.  
US6057427-A.  
02-MAY-2000.  
05-JUN-1996; 96US-00652446.  
20-NOV-1991; 91US-00796066.  
10-AUG-1993; 93US-00104736.  
27-OCT-1994; 94US-00330108.  
05-JUN-1996; 96MO-US008992.  
(DART-) DARTMOUTH COLLEGE.

Beading C, Smith KA;  
MPI: 2000-338623/29.  
N-PSDB; AAA39665.

Novel antibody or antibody fragment which selectively binds to a polypeptide encoded by cytokine response gene 2.

Example IV; Col 99-100; 66pp; English.

This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence represents the human CR6 protein described in the invention

Sequence 159 AA;

Query Match 100.0%; Score 826; DB 3; Length 159;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89; Indels 0; Gaps 0;  
Matches 159; Conservative 0; Mismatches 0;

```
QY 1 MTLSEVRGDDTVPESTARMOGAKALHELLLSAQRQGCCTAGYSAKYLVNDPNDVTRC 60
DB 1 MTLSEVRGDDTVPESTARMOGAKALHELLLSAQRQGCCTAGYSAKYLVNDPNDVTRC 60
QY 61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVQRLAIVAGGEAGAPGDLHCT 120
DB 61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVQRLAIVAGGEAGAPGDLHCT 120
QY 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
DB 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
```

RESULT 3  
ABR40340  
ID ABR40340 standard; protein; 159 AA.  
XX  
AC ABR40340;  
XX  
DT 04-JUL-2003 (first entry)  
XX  
DE Human Gadd45 SEQ ID NO: 10.  
XX  
DE Human Gadd45  
XX  
KW Human; c-Jun-N-terminal kinase pathway; JNK pathway; cytostatic; programmed cell death; TNFalpha; Fas; TRAIL; genotoxic agent; cancer; apoptosis; Gadd45beta; JNK2; chronic inflammatory disease; Gadd45; autoimmune condition.  
OS Homo sapiens.  
XX  
PN MO2003028659-A2.  
XX  
PD 10-APR-2003.  
XX  
PF 02-OCT-2002; 2002MO-US031548.  
XX  
PR 02-OCT-2001; 2001US-0326492P.  
XX  
PR 12-OCT-2001; 2001US-0328811P.  
XX  
PA (UYCH-) UNIV CHICAGO.  
XX  
PI Franzoso G, De Smaele E, Zazzeroni F, Papa S;  
XX  
DR MPI: 2003-430155/40.  
XX  
DR N-PSDB; ACC59049.

Modulating pathways leading to programmed cell death, by selecting a target within Jun-N-terminal kinase pathway and interfering with the target using agent that up or down regulates the JNK pathway.

PS Disclosure; Page 122-123; 13pp; English.  
XX  
XX The invention relates to a novel method for modulating pathways leading to programmed cell death, comprising selecting a target within the c-Jun-N-terminal kinase (JNK) pathway, and interfering with the target using an agent that either up regulates or down regulates the JNK pathway. The method of the invention has cytostatic activity. A method of the invention is useful for modulating pathways leading to programmed cell death induced by TNFalpha, Fas, TRAIL, genotoxic agent such as demorubicin or cisplatin. Another method of the invention is useful for screening and identifying an agent, preferably peptides, peptide mimetics, peptide-like molecules, mutant proteins, cDNAs, antisense oligonucleotides or constructs, lipids, carbohydrates or synthetic or natural chemical compounds, that modulate JNK pathway in vitro. A method of the invention may also be useful for treating cancer, and for preventing apoptosis. Compounds that are capable of interfering with the ability of Gadd45beta to associate with JNK2 are useful for treating

human diseases such as chronic inflammatory, and autoimmune conditions and certain types of cancer. The present sequence is used in the exemplification of the invention

Sequence 159 AA;

Query Match 100.0%; Score 826; DB 6; Length 159;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 MTLSEVRGQDTVPPESTARWQAGAKALHELLLSAQRQCCTTAQVYESAKYLVNDPNDVTC 60
1 MTLSEVRGQDTVPPESTARWQAGAKALHELLLSAQRQCCTTAQVYESAKYLVNDPNDVTC 60
61 VIAAGEBEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIYVAGEEAGAPGDLHCI 120
61 VIAAGEBEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIYVAGEEAGAPGDLHCI 120
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

```

ADG62828 standard; protein; 159 AA.

ADG62828;

11-MAR-2004 (first entry)

Human growth arrest and DNA-damage-inducible gamma protein.

Growth arrest and DNA damage-inducible gene 45; GADD45; Cdc2; cell division cycle-2; DNA repair; cancer; DNA-damaging agent; therapy; chemotherapeutic agent; cis-platin; apoptosis; cytostatic; human.

Homo sapiens.

US6613318-B1.

02-SEP-2003.

24-MAR-2000; 2000US-00534811.

25-MAR-1999; 99US-0126069P.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Wang XM, Harris CC, Fornace AJ, Coursen JD, Zhan Q;

WPI; 2003-895366/82.

In vitro identification of GADD45 modulators, useful for increasing sensitivity of cancer cells to DNA damage, e.g. from effects of compounds on GADD45 binding.

Disclosure; SEQ ID NO 7; 37pp; English.

The present invention relates to a novel method for assaying modulators of growth arrest and DNA damage-inducible (GADD) 45 proteins. The method involves incubating the compound with GADD45 in aqueous solution and determining any inhibition or decrease in the binding of GADD45 specifically to a Cdc2 (cell division cycle-2) polypeptide. Inhibition of GADD45, a protein involved in DNA repair, results in increased sensitivity of cancer cells to DNA-damaging agents. GADD45 activates a G2/M checkpoint after damage induced by UV radiation or alkylating agents and overexpression of GADD45 in normal fibroblasts arrests cells in G2/M. Compounds that inhibit GADD45 are able to sensitize proliferating cells to DNA-damaging agents, so are useful as adjuncts in treatment of cancer with UV light or chemotherapeutic agents such as cis-platin. Inhibition of GADD45 will allow a reduction in the dose of toxic DNA-damaging agents required to induce apoptosis in cancer cells. The present sequence is

CC human GADD45 gamma protein.

XX Sequence 159 AA;

Query Match 100.0%; Score 826; DB 7; Length 159;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 MTLSEVRGQDTVPPESTARWQAGAKALHELLLSAQRQCCTTAQVYESAKYLVNDPNDVTC 60
1 MTLSEVRGQDTVPPESTARWQAGAKALHELLLSAQRQCCTTAQVYESAKYLVNDPNDVTC 60
61 VIAAGEBEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIYVAGEEAGAPGDLHCI 120
61 VIAAGEBEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIYVAGEEAGAPGDLHCI 120
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

```

ADP65201 standard; protein; 159 AA.

ADP65201;

12-AUG-2004 (first entry)

Human growth arrest and damage-inducible, gamma, GADD45-gamma.

autoimmune disease; arthritis; gene expression analysis; rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antigout; antiinflammatory; dermatological; immunomodulatory; lupus; ankylosing spondylitis; fibrositis; fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis; immune; human.

Homo sapiens.

WO2003072827-A1.

04-SEP-2003.

31-OCT-2002; 2002WO-US035433.

31-OCT-2001; 2001US-0336220P.

(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

Hirsch R, Thorton SL;

WPI; 2003-712740/67.

GENBANK; NP\_006696.

Diagnosing and analyzing autoimmune disease using gene expression profiles and microarray technology, useful for diagnosing and treating rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and gout.

Disclosure; Page; 56pp; English.

The invention relates to a novel method for diagnosing and analysing autoimmune disease or arthritides. The method comprises obtaining a patient sample containing mRNA, analysing gene expression using the mRNA that results in a gene expression signature of the mRNA, and using that gene expression signature to diagnose or analyse the autoimmune disease or arthritides in the patient, where gene expression of at least 60% of the genes correlates with that of the gene signature. The invention further comprises: a treatment of rheumatoid arthritis; identification of genes for targeting in the treatment of rheumatoid arthritis in a mammal other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an array or gene chip, specific for rheumatoid arthritis; diagnosis or

analyses of autoimmune disease or rheumatoid arthritis; screening the efficacy of a candidate drug in vitro for the treatment of collagen-induced arthritis; and reducing the symptoms associated with collagen-induced arthritis. The compositions of the invention have the following activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic, antiinflammatory, dermatological, and immunomodulatory. The methods and compositions of the present invention are useful for diagnosing and treating autoimmune disease or arthritis, such as rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis, fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an immune disease caused by an infectious agent. This sequence represents a protein sequence relating to the genes used in the analysis and treatment of autoimmune diseases or arthritis. Note: This sequence is not shown in the specification. It has been supplied in an electronic format from WIP0.

Sequence 159 AA;

ry Match 100.0%; Score 826; DB 7; Length 159;  
c Local Similarity 100.0%; Pred. No. 3.7e-89;  
ches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLSEVRGDDTPESTARMQAGKALHELLLSAOROGCTTAGVYESAKYLVNDPNDVTPC 60  
1 MTLSEVRGDDTPESTARMQAGKALHELLLSAOROGCTTAGVYESAKYLVNDPNDVTPC 60  
61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIVAGSEBAGAPGDLHCI 120  
61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIVAGSEBAGAPGDLHCI 120

121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

T 6  
308  
ADJ75308 standard; protein; 159 AA.

ADJ75308;

20-MAY-2004 (first entry)

Marker gene related amino acid sequence SEQ ID NO:560.

bronchial asthma; chronic obstructive pulmonary disease;  
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
gene therapy; marker.

Homo sapiens.

EP1394274-A2.

03-MAR-2004.

04-AUG-2003; 2003EP-00254857.

06-AUG-2002; 2002JP-00229312.  
20-MAR-2003; 2003JP-00077212.

(GENO-) GENOX RES INC.

Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

WPI; 2004-193155/19.

Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.

Example 11; SEQ ID NO 560; 241pp; English.

CC The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic  
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
CC genes (S1) whose expression levels increase when respiratory epithelial  
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
CC whose expression levels decrease when respiratory epithelial cells are  
CC stimulated with interleukin-13. Also described: (1) a reagent (1) for  
CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
CC (2) a kit for screening for a candidate compound for a therapeutic agent  
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
CC an animal model for bronchial asthma or chronic obstructive pulmonary  
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
CC method for producing an animal model for bronchial asthma or chronic  
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
CC a marker gene or an antisense nucleic acid corresponding to a portion of  
CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
CC expression of the gene through an RNAi effect or an antibody recognising  
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
CC probe has been immobilised to assay a marker gene. (1) has respiratory  
CC and antiasthmatic activities, and can be used in gene therapy. The method  
CC is useful for testing for or screening for a therapeutic agent for  
CC bronchial asthma or chronic obstructive pulmonary disease. The present  
CC sequence is used in the exemplification of the present invention.

Sequence 159 AA;

ry Match 100.0%; Score 826; DB 8; Length 159;  
Best Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLSEVRGDDTPESTARMQAGKALHELLLSAOROGCTTAGVYESAKYLVNDPNDVTPC 60  
DB 1 MTLSEVRGDDTPESTARMQAGKALHELLLSAOROGCTTAGVYESAKYLVNDPNDVTPC 60

QY 61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIVAGSEBAGAPGDLHCI 120  
DB 61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIVAGSEBAGAPGDLHCI 120

QY 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
DB 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

RESULT 7

ID ADX85166 standard; protein; 159 AA.

AC ADX85166;

DT 05-MAY-2005 (first entry)

DE Human gadd45 protein, seqid:10.

KW Cell death; apoptosis; degeneration; cancer; cytostatic; neoplasia;  
KW immunotherapy; chemotherapy; gene therapy; gadd45;  
KW Jun N terminal kinase modulator.

OS Homo sapiens.

PN EP1506784-A1.

PD 16-FEB-2005.

PF 26-JUL-2004; 2004EP-00017667.

PR 25-JUL-2003; 2003US-00626905.  
PR 02-DEC-2003; 2003US-0526231P.

(UYCH-) UNIV CHICAGO.

Franoso G, Desmaele E, Zazzeroni F, Papa S, Bubici C;

WPI; 2005-154742/17.  
N-PSDB; ADX85165.

Method for modulating pathways leading to programmed cell death for treating cancer. By obtaining peptide having specific amino acid sequence and regulating JNK pathway using peptide or composition developed using peptide sequence.

Example 14; SEQ ID NO 10; 110pp; English.

The invention relates to methods and compositions for modulating pathways leading to programmed cell death or apoptosis. The method involves selecting a target within the c-Jun-N-terminal Kinase (JNK) pathway and interfering the target by an agent that either upregulates or downregulates the JNK pathway. The JNK modulator is effective in treating degenerative disease and cancer. The method and compositions of the invention are useful in immunotherapy, cancer chemotherapy and in gene therapy. The present sequence is the human gadd45 protein which is a modulator of JNK pathway.

Sequence 159 AA:

Query Match 100.0%; Score 826; DB 9; Length 159;  
Local Similarity 100.0%; Pred. No. 3.7e-89;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 MTLLEEVAGQDTPVPESTARMOGAGKALHELLLSAQRQCLTAGVYESAKVLNVDNDNTFC 60
1 MTLLEEVAGQDTPVPESTARMOGAGKALHELLLSAQRQCLTAGVYESAKVLNVDNDNTFC 60
61 VLAAGEDEBDIALQIHFTLLOAFCCENDIDIVRGVORLAIVGAGEAGAGDHLHI 120
61 VLAAGEDEBDIALQIHFTLLOAFCCENDIDIVRGVORLAIVGAGEAGAGDHLHI 120
121 LISNPNEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
121 LISNPNEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
121 LISNPNEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

```

i.T. 8  
4299  
AED74299 standard; protein; 165 AA.  
AED74299;

12-JAN-2006 (first entry)

Human placental protein SEQ ID NO:1127.

pre-eclampsia; gynecological.

Homo sapiens.

US2005255114-A1.

17-NOV-2005.

07-APR-2004; 2004US-00821224.

07-APR-2003; 2003US-0462047P.

(NUVE-) NUVELO INC.

Labat I, Tang YT, Staechle-Crain B, Boyle B;

WPI; 2005-808574/82.  
N-PSDB; AED73447.

PT Identifying a patient with a higher risk of preeclampsia comprises  
PT nucleic acid hybridization assay or antibody assay to determine level of  
PT a specific nucleic acid (mRNA) or polypeptide.

Claim 2; SEQ ID NO 1127; 358pp; English.

The invention relates to a method for identifying a patient with a higher risk of preeclampsia. The method comprises: (a) assaying a sample from the patient to determine the level of a mRNA or other polynucleotide within the sample that hybridizes specifically to a polynucleotide of AED73173-AED74024, and comparing the level to a standard; or (b) contacting a sample from the patient with an antibody that specifically binds to a polypeptide of AED74025-AED74876 to determine the level of polypeptide within the sample, and comparing the level to a standard. Also described: (1) a diagnostic kit, for detecting preeclampsia, comprising: (a) an antibody specific for any of the polypeptides of AED74025-AED74876 or their fragments; or (b) a polynucleotide sequence comprising any of AED73173-AED74024 coupled to a surface; and (c) a standard for any of the polypeptides of AED74025-AED74876 or any of the polynucleotides of AED73173-AED74024 indicative of a higher risk of preeclampsia. (2) a pharmaceutical composition comprising an antibody specific for any of the polypeptides of AED74025-AED74876 or one or more purified polypeptides of AED74025-AED74876, to ameliorate signs or symptoms of preeclampsia; and (3) a method of treating preeclampsia. The method and kit are useful for identifying a patient with a higher risk of preeclampsia. The composition and method are useful for treating preeclampsia. The present sequence represents an amino acid sequence encodes by a nucleic acid sequence obtained from a human placental cDNA library. Note - The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.

Sequence 165 AA:

Query Match 100.0%; Score 826; DB 9; Length 165;  
Best Local Similarity 100.0%; Pred. No. 3.9e-89;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 MTLLEEVAGQDTPVPESTARMOGAGKALHELLLSAQRQCLTAGVYESAKVLNVDNDNTFC 60
7 MTLLEEVAGQDTPVPESTARMOGAGKALHELLLSAQRQCLTAGVYESAKVLNVDNDNTFC 66
61 VLAAGEDEBDIALQIHFTLLOAFCCENDIDIVRGVORLAIVGAGEAGAGDHLHI 120
67 VLAAGEDEBDIALQIHFTLLOAFCCENDIDIVRGVORLAIVGAGEAGAGDHLHI 126
121 LISNPNEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
127 LISNPNEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 165

```

RESULT 9  
AAB13772  
ID AAB13772 standard; protein; 160 AA.

AAB13772;

20-JUN-2001 (first entry)

Human SYG972 protein.

Human; SYG972; cancer diagnosis; cell differentiation; cytostatic;  
breast cancer; lymphoma; Alzheimer's disease; Parkinson's disease;  
degenerative nervous disease.

Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 58 /note= "Encoded by ACC"

FT Misc-difference 68 /note= "Encoded by GAC"

FT Misc-difference 160

/note= "Encoded by TGA"

W0200036147-A1.

22-JUN-2000.

09-DEC-1999; 99WO-KR000756.

12-DEC-1998; 98KR-00054933.

30-DEC-1998; 98KR-00063958.

(SAMT-) SAMYANG GENEX CORP.

Jung N, Kim JM, Yi Y, Bae I, Hong S, Lee H;

NPI; 2000-431614/37.

N-PSDB; AAA64826, AAA64827.

Diagnosis of cancer using a probe comprising all or part of an SYG972 gene.

Example 1; Page 24-25; 31pp; English.

The present sequence is the protein sequence for the human SYG972 gene. SYG972 protein is involved in cell differentiation. SYG972 gene is highly expressed in normal differentiated tissues. However, in cancerous tissues, SYG972 gene expression is inhibited. This characteristic of SYG972 gene expression may be used in cancer diagnosis, especially breast cancer. In addition, the SYG972 gene may be used in distinguishing B cells and T cells in determining the origin of cancer in various lymphomas. SYG972 gene and promoter are useful for designing and screening drugs to promote or inhibit apoptosis and differentiation of cells, especially to screen drugs to treat diseases where cell differentiation and apoptosis occur abnormally e.g. cancer, Alzheimer's disease, Parkinson's disease and degenerative nervous diseases

Sequence 160 AA;

TY Match 98.2%; Score 811; DB 3; Length 160;  
c Local Similarity 98.7%; Pred. No. 2.2e-87;  
ches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

1 MTLSEVRGDDTVPESTARMOGAGKALHELLLSAQRGGCTTAGVYESAKYLVNDPDPVTRC 60
|||||
1 MTLSEVRGDDTVPESTARMOGAGKALHELLLSAQRGGCTTAGVYESAKYLVNDPDPVTRC 60
61 VLAAGEDEGDIATLQIHFTLQAFCCENDIDIVRVGVORLAIYVGAEGAGAPGDLHCT 120
|||||
121 LISNPEDAMKDPALFKSLFCESRSVNDWVPSTLPE 159
|||||
121 LISNPEDAMKDPALFKSLFCESRSVNDWVPSTLPE 159
121 LISNPEDAMKDPALFKSLFCESRSVNDWVPSTLPE 159

```

T 10

533

AAW23533 standard; protein; 159 AA.

AAW23533;

17-FEB-1998 (first entry)

Human GRP17 associated with cell growth arrest and DNA damage.

GRP17 gene; Gadd45 and MyD118 related protein; human;  
cell growth arrest; DNA damage; cancer; apoptosis; autoimmune disease;  
diagnosis; therapy; antibody.

Homo sapiens.

Key Location/Qualifiers  
Region 40..69

/note= "region of high homology with gadd45 and MyD118 "

XX EP787798-A2.

XX 06-AUG-1997.

XX 10-FEB-1997; 97EP-00102108.

XX 09-FEB-1996; 96JP-00023612.

XX (SAKA ) OTSUKA PHARM CO LTD.

XX Suzuki M, Watanabe T, Fujiwara T;

XX WPI; 1997-387484/36.

XX N-PSDB; AAT74047, AAT74048.

PT New GRP17 gene associated with arrest of cell growth and induction of DNA  
PT damage - useful for diagnosis and treatment of cancer, auto-immune  
PT diseases etc., also for drug screening.

PS Claim 1; Page 8; 12pp; English.

CC This protein comprises novel human GRP17 (Gadd45 and MyD118 related  
CC protein, 17 kDa), a protein encoded by a gene associated with arrest of  
CC cell growth and induction of DNA damage. The amino acid sequence was  
CC deduced from cDNA clone GEN-554H06 (see AAT74047-48) isolated from a  
CC human placental cDNA library. GRP17 protein shows 55% identity with  
CC gadd45 and 52% identity with MyD118, both of which are tumour  
CC suppressors. It can be expressed in the usual vector/host cell systems.  
CC The GRP17 gene is useful for the diagnosis and treatment of cancer,  
CC malformations and autoimmune diseases, as well as for screening drugs for  
CC treatment of these conditions. Recombinant GRP17 protein can be used to  
CC raise antibodies for the purification, assay and identification of GRP17  
CC proteins

SQ Sequence 159 AA;

Query Match 97.3%; Score 804; DB 2; Length 159;  
Best Local Similarity 98.1%; Pred. No. 1.5e-86;  
Matches 156; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 MTLSEVRGDDTVPESTARMOGAGKALHELLLSAQRGGCTTAGVYESAKYLVNDPDPVTRC 60
|||||
Db 1 MTLSEVRGDDTVPESTARMOGAGKALHELLLSAQRGGCTTAGVYESAKYLVNDPDPVTRC 60
61 VLAAGEDEGDIATLQIHFTLQAFCCENDIDIVRVGVORLAIYVGAEGAGAPGDLHCT 120
|||||
QY 121 LISNPEDAMKDPALFKSLFCESRSVNDWVPSTLPE 159
|||||
Db 121 LISNPEDAMKDPALFKSLFCESRSVNDWVPSTLPE 159
121 LISNPEDAMKDPALFKSLFCESRSVNDWVPSTLPE 159

```

RESULT 11

ABR40341

ID ABR40341 standard; protein; 159 AA.

XX ABR40341;

XX 04-JUL-2003 (first entry)

XX Mouse Gadd45 SEQ ID NO: 12.

XX Mouse; c-Jun-N-terminal kinase pathway; JNK pathway; cytosolic;  
XX programmed cell death; TNFalpha; Fas; TRAIL; genotoxic agent; cancer;  
XX apoptosis; Gadd45beta; JNK2; chronic inflammatory disease; Gadd45;  
XX autoimmune condition.

XX Mus musculus.

XX W020003028659-A2.



10-APR-2003.  
02-OCT-2002; 2002WO-US031548.  
02-OCT-2001; 2001US-0326492P.  
12-OCT-2001; 2001US-0328811P.  
(UYCH-) UNIV CHICAGO.  
Franzoso G, De Smaele E, Zazzeroni F, Papa S;  
WPI; 2003-430155/40.  
N-PSDB; ACCS9050.  
Modulating pathways leading to programmed cell death, by selecting a target within Jun-N-terminal kinase pathway and interfering with the target using agent that up or down regulates the JNK pathway.  
Disclosure; Page 124; 131pp; English.

The invention relates to a novel method for modulating pathways leading to programmed cell death, comprising selecting a target within the c-Jun-N-terminal kinase (JNK) pathway, and interfering with the target using an agent that either up regulates or down regulates the JNK pathway. The method of the invention has cytostatic activity. A method of the invention is useful for modulating pathways leading to programmed cell death induced by TNFalpha, Fas, TRAIL, genotoxic agent such as doxorubicin or cisplatin. Another method of the invention is useful for screening and identifying an agent, preferably peptides, peptide mimetics, peptide-like molecules, mutant proteins, cDNAs, antisense oligonucleotides or constructs, lipids, carbohydrates or synthetic or natural chemical compounds, that modulate JNK pathway in vitro. A method of the invention may also be useful for treating cancer, and for preventing apoptosis. Compounds that are capable of interfering with the ability of Gadd45beta to associate with JNK2 are useful for treating human diseases such as chronic inflammatory, and autoimmune conditions and certain types of cancer. The present sequence is used in the exemplification of the invention

Sequence 159 AA;

Query Match 95.3%; Score 787; DB 6; Length 159;  
Best Local Similarity 95.6%; Pred. No. 1.6e-84;  
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

1 MTLSEVRGQDTVESTRMKGAGALHELLLSAQRQCTAGVYESAKVNVDPDNTFC 60
1 MTLSEVRGQDTVESTRMKGAGALHELLLSAQRQCTAGVYESAKVNVDPDNTFC 60
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRVGVQRLAIVGABEAGAPGDLHCT 120
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRVGVQRLAIVGABEAGAPGDLHCT 120
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRVGVQRLAIVGABEAGAPGDLHCT 120
121 LISNPNEDTWKDPALFKLSLFCESRSFNDWVPSITLPE 159

```

Query Match 95.3%; Score 787; DB 6; Length 159;  
Best Local Similarity 95.6%; Pred. No. 1.6e-84;  
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ADJ76135;

20-MAY-2004 (first entry)

Marker gene related amino acid sequence SEQ ID NO:1387.  
bronchial asthma; chronic obstructive pulmonary disease;  
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
gene therapy; marker.

OS Mus musculus.  
XX EPI394274-A2.  
XX 03-MAR-2004.  
XX 04-AUG-2003; 2003EP-00254857.  
XX 06-AUG-2002; 2002JP-00229312.  
XX 20-MAR-2003; 2003JP-00077212.  
XX (GENO-) GENOX RES INC.  
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;  
XX WPI; 2004-193155/19.  
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
XX comparing the expression level of a marker gene in a biological sample  
XX from a subject with the expression level of the gene in a sample from a  
XX healthy subject.  
XX Claim 16; SEQ ID NO 1387; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

Sequence 159 AA;

Query Match 95.3%; Score 787; DB 6; Length 159;  
Best Local Similarity 95.6%; Pred. No. 1.6e-84;  
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

1 MTLSEVRGQDTVESTRMKGAGALHELLLSAQRQCTAGVYESAKVNVDPDNTFC 60
1 MTLSEVRGQDTVESTRMKGAGALHELLLSAQRQCTAGVYESAKVNVDPDNTFC 60
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRVGVQRLAIVGABEAGAPGDLHCT 120
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRVGVQRLAIVGABEAGAPGDLHCT 120
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRVGVQRLAIVGABEAGAPGDLHCT 120
121 LISNPNEDTWKDPALFKLSLFCESRSFNDWVPSITLPE 159

```

T 13  
168  
ADX85168 standard; protein; 159 AA.  
ADX85168;

05-MAY-2005 (first entry)

Mouse gadd45 protein, seqid:12.

Cell death; apoptosis; degeneration; cancer; cytostatic; neoplasm;  
immunotherapy; chemotherapy; gene therapy; gadd45;  
Jun N terminal kinase modulator.

Mus musculus.

EPI506784-A1.

16-FEB-2005.

26-JUL-2004; 2004EP-00017667.

25-JUL-2003; 2003US-00626905.  
02-DEC-2003; 2003US-0526231P.

(UYCH-) UNIV CHICAGO.

Franzoso G, Desmaele E, Zazzeroni F, Papa S, Bubici C;

WPI; 2005-154742/17.  
N-PSDB; ADX85167.

Method for modulating pathways leading to programmed cell death for  
creating cancer, by obtaining peptide having specific amino acid sequence  
and regulating JNK pathway using peptide or composition developed using  
peptide sequence.

Example 14; SEQ ID NO 12; 110pp; English.

The invention relates to methods and compositions for modulating pathways  
leading to programmed cell death or apoptosis. The method involves  
selecting a target within the c-Jun-N-terminal kinase (JNK) pathway and  
interfering the target by an agent that either upregulates or  
downregulates the JNK pathway. The JNK modulator is effective in treating  
degenerative disease and cancer. The method and compositions of the  
invention are useful in immunotherapy, cancer chemotherapy and in gene  
therapy. The present sequence is the mouse gadd45 protein which is a  
modulator of JNK pathway.

Sequence 159 AA;

RY Match 95.3%; Score 787; DB 9; Length 159;

c Local Similarity 95.6%; Pred. No. 1.6e-84;  
ches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```

1 MTLSEVRGQDTPESTRARMOGAKALHELLLSAQRQCLTAGYBSAKVLNVPDNTFC 60
1 MTLSEVRGQDTPESTRARMOGAKALHELLLSAQRQCLTAGYBSAKVLNVPDNTFC 60
1 MTLSEVRGQDTPESTRARMOGAKALHELLLSAQRQCLTAGYBSAKVLNVPDNTFC 60
61 VLAAGEDEBDIALQIHTLIQAFCCENDIDIVRGVORLAAIVGAGEAGAPGDLHCI 120
61 VLAAGEDEBDIALQIHTLIQAFCCENDIDIVRGVORLAAIVGAGEAGAPGDLHCI 120
61 VLAAGEDEBDIALQIHTLIQAFCCENDIDIVRGVORLAAIVGAGEAGAPGDLHCI 120
121 LISNPEDAWKDPALFKLSLFCESRSRVNDVPSITLPE 159
121 LISNPEDAWKDPALFKLSLFCESRSRVNDVPSITLPE 159
121 LISNPEDAWKDPALFKLSLFCESRSRVNDVPSITLPE 159

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T 14  
647  
ABM85647 standard; protein; 141 AA.

ABM85647;

```

XX 18-NOV-2004 (first entry)
DT Human protein sequence hCP1767168.
XX
DE Human protein sequence hCP1767168.
XX
XX Cytostatic; carcinoma; lymphoma; cancer; human.
XX
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
PT comprises a nucleotide sequence.
XX
PS Claim 5; SEQ ID NO 1356; Opp; English.
XX
XX The present invention relates to novel DNA and protein sequences which
XX are associated with carcinomas. The sequences are useful for: (i) for
XX screening drug candidates; (ii) for screening of bioactive agent capable
XX of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
XX a bioactive agent capable of modulating the activity of CAP; (iv) for
XX evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
XX carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
XX carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
XX (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
XX determining Carcinoma Associated (CA) gene copy number. In addition, the
XX CA genes are useful as DNA vaccines and the CAP are useful as markers of
XX carcinoma including lymphoma. The present sequence is one such CAP. Note:
XX This patent is an equivalent to basic patent US2002182586A1, for which no
XX sequence data was published
SQ
SQ Sequence 141 AA;
Query Match 89.2%; Score 737; DB 7; Length 141;
Best Local Similarity 100.0%; Pred. No. 1.1e-78;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 MOGAKALHELLLSAQRQCLTAGYBSAKVLNVPDNTFCVLAAGEDEBDIALQIHF 78
DB 1 MOGAKALHELLLSAQRQCLTAGYBSAKVLNVPDNTFCVLAAGEDEBDIALQIHF 60
QY 79 TLIQAFCCENDIDIVRGVORLAAIVGAGEAGAPGDLHCILISNPEDAWKDPALFKL 138
DB 61 TLIQAFCCENDIDIVRGVORLAAIVGAGEAGAPGDLHCILISNPEDAWKDPALFKL 120
QY 139 SLFCESRSRVNDVPSITLPE 159
DB 121 SLFCESRSRVNDVPSITLPE 141
RESULT 15
ADV77059
ID ADV77059 standard; protein; 185 AA.
XX
AC ADV77059;
XX
XX 10-MAR-2005 (first entry)
DT Huntingtons chorea interaction partner #20.
XX
DE Huntingtons chorea interaction partner #20.
XX
XX genetic disorder; neurological disease; Nootropic; Anticonvulsant;
XX

```

Huntingtons chorea; protein structure.

**Homo sapiens.**

WO2004113566-A2.

29-DEC-2004

18-JUN-2004; 2004WO-EP006617.

20-JUN-2003; 2003EP-00013957.

(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN  
(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

(DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.

Wanker E, Lehnach H, Goehler H, Stroedicke M, Stelzl U, Lalowski M;

Lałowski M;

WPI; 2005-057993/06.

Generating a protein-interaction network of huntingtin, useful for diagnosing and treating Huntington's disease, comprises contacting (poly)peptides with the disease-related (poly)peptides.

Disclosure; Fig 6; 161pp; English.

The invention relates to a method of generating a network of direct and indirect interaction partners of a disease-related (poly)peptide comprising contacting a selection of (poly)peptides suspected to contain direct or indirect interaction partners with the disease-related (poly)peptides and optionally with known direct or indirect interaction partners of the disease-related (poly)peptide. The molecule, (poly)peptide, and antibody are useful for preparing a pharmaceutical composition for the treatment of Huntingtons chorea. The method is useful for generating a network of direct and indirect interaction partners of a disease-related (poly)peptide. The protein, composition, and methods are useful for diagnosing and treating Huntingtons chorea. The present sequence represents the amino acid sequence of an interaction partner of Huntingtons chorea.

Sequence 185 AA;

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try Match      88.1%; Score 728; DB 9; Length 185;
at Local Similarity 98.6%; Pred. No. 1.9e-77;
ches 140; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Local Similarity 98.6%; Pred. No. 1.9e-77;  
 Mismatches 140; Conservative 0; Mismatches 2

Matches 140; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

18 RMGGACKATHELLSAOROGCLTAGVYESAKVLNVDPNVTFCVLAGEEDEGDIALQIH 77

44 RMGAKALHELLSAQRQCLTAGVYESAKVLNVDPDNVTFCVLAAGEEDEGDIALQIH 103

78 FTLIQAFCCENDIDIVRGDVQRLAIVGAGEEAGAPGDLHCILISNPNEADAWKDPAAEK 137

104 FTLLQAFCCENDIDIVRGDVQRLAIVGAGEAGAPGDLHCILISNPNEADAWKDPAAEK 163

138 LSLFCEESRVNDWVPSITLPE 159

164 LSLFCEESRSVNDWVPSITLPE 185

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Job completed: June  2, 2006, 22:34:19
Time : 92 secs

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Time : 92 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

rotein - protein search, using sw model

June 2, 2006, 22:34:30 ; Search time 22 Seconds  
(without alignments)  
695.385 Million cell updates/sec

US-10-089-641-2

act score: 826  
1 MTLSEVRGQDVTPESTARMQ.....LFCESRSVNDWVPSITLPE 159

ng table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

hed: 283416 segs, 96216763 residues

number of hits satisfying chosen parameters: 283416

um DB seq length: 0  
um DB seq length: 200000000

processing: Minimum Match 0%

Maximum Match 100%

ase :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Score	Query	Match	Length	DB	ID	Description
463.5	56.1	165	2	B39617		DNA-damage-inducib
463.5	56.1	165	2	I48111		DNA-damage-inducib
457.5	55.4	165	2	A39617		DNA-damage-inducib
451.5	54.7	165	2	B56535		DNA-damage-inducib
436.5	52.8	165	2	S68690		GADD45 protein - r
436.5	52.8	160	2	A43813		MD118 protein - r
103.5	12.5	132	1	JC4159		ribosomal protein
101.5	12.5	132	1	I51557		ribosomal protein
101	12.2	145	2	T41651		408 ribosomal prot
94	11.4	349	2	A97124		recombinat prot
94	11.4	349	2	D84577		probable reca prot
93.5	11.3	132	1	R3MS12		ribosomal protein
93.5	11.3	132	1	R3RT12		ribosomal protein
91	11.0	145	2	JN0639		recombinat prot
87.5	10.6	145	2	TJ4303		hypothetical prote
86.5	10.5	132	1	R3H012		ribosomal protein
85.5	10.4	134	2	S08222		recombinat prot
85	10.3	1184	2	H86190		hypothetical prote
83	10.0	347	1	H89902		Reca protein (limpo
82.5	10.0	346	1	RQPSA		Reca protein PA161
82.5	10.0	355	1	RQEBM		recombination prot
82.5	10.0	907	2	D83427		probable transcrip
82	9.9	331	2	A42602		recombination prot
82	9.9	349	2	G83947		multifunctional pr
81.5	9.9	349	2	JN0321		recombination prot
81.5	9.9	352	2	A47709		recombination prot
81.5	9.9	352	2	JC2406		recombination prot
81.5	9.9	357	2	A12214		recombination prot
81	9.8	353	2	AH0843		Reca protein (limpo

30	81	9.8	374	2	T35139	reca protein - Str
31	81	9.8	374	2	S38674	recombination prot
32	80.5	9.7	144	1	S24781	ribosomal protein
33	80.5	9.7	354	2	S31481	recombination prot
34	80.5	9.7	355	2	T10482	reca protein - pse
35	80.5	9.7	356	2	S37586	recombination prot
36	80.5	9.7	356	2	AG0401	Reca protein (limpo
37	80.5	9.7	790	2	S18206	recombination prot
38	80.5	9.7	1637	2	T00070	hypothetical prote
39	80	9.7	213	2	T39518	40s ribosomal prot
40	80	9.7	213	2	H83552	conserved hypothet
41	80	9.7	318	2	J00758	recombination prot
42	80	9.7	353	1	RQPCA	recombination prot
43	80	9.7	353	1	D91073	Reca protein (limpo
44	79.5	9.6	151	2	S58022	ribosomal protein
45	79.5	9.6	358	1	ROA1A	recombination prot

#### ALIGNMENTS

RESULT 1  
B39617  
DNA-damage-inducible protein gadd45 - Chinese hamster  
C/Species: Cricetus griseus (Chinese hamster)  
C/Date: 13-Sep-1991 #sequence\_revision 13-Sep-1991 #ext\_change 11-Jan-2000  
C/Accession: B39617  
R/Papathanasiou, M.A.; Kerr, N.C.K.; Robbins, J.H.; McBride, O.W.; Alamo Jr., I.; Barre  
Mol. Cell. Biol. 11, 1009-1016, 1991  
A/Title: Induction by ionizing radiation of the gadd45 gene in cultured human cells: 1a  
A/Reference number: A39617, MID:91117202, PMID:1990262  
A/Accession: B39617  
A/Molecule type: mRNA  
A/Residues: 1-165 <PAP>  
A/Cross-references: UNIPARC:UP1000012AF8B; GB:M60973; NID:g191079; PIDN:AAA36984.1; PID  
C/Note: the source is Chinese hamster ovary cells  
C/Superfamily: human DNA-damage-inducible protein gadd45

Query Match  
Best Local Similarity 56.1%; Score 463.5; DB 2; Length 165;  
Best Local Similarity 55.1%; Pred. No. 3.2e-37;  
Matches 92; Conservative 23; Mismatches 41; Indels 11; Gaps 3;

QY 1 MTLSEVRGQDVTPESTARMQAGKALHELLSROGCLFAGYSESATVNDPNDVTF 60  
DB 1 MTLSEFSAAE---OKTERMDVTGDALEEVLSKRSQRTTVGYEAKKLNVDPDNYLC 57

QY 61 VLAAGEDEGDIALQIHFTLQAFCCENDIDYRVGDVORLAIV-----GAGEBAGA- 113  
DB 58 LLADEDDDDVALQIHFTLQAFCCENDINIRVSPGLAELLLESDDAGPESGGAS 117

QY 114 -PGDLHCILISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
DB 118 QPDLHCILVLTNPSSQWKPALSLQILCFRESRYMQWVPVINTLPE 164

RESULT 2  
I48111  
DNA-damage-inducible protein gadd45 - long-tailed hamster  
C/Species: Cricetus longicaudatus (long-tailed hamster)  
C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #ext\_change 09-Jul-2004  
C/Accession: I48111  
R/Hollander, M.C.; Alamo, I.; Jackman, J.; Wang, M.G.; McBride, O.W.; Fornace, A.J.  
J. Biol. Chem. 268, 24385-24393, 1993  
A/Title: Analysis of the mammalian gadd45 gene and its response to DNA damage.  
A/Reference number: I48111, MID:94043278; PMID:8226988  
A/Accession: I48111  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-165 <RES>  
A/Cross-references: UNIPROT:P24523; UNIPARC:UP1000012AF8B; GB:L25339; NID:g409032; PIDN  
C/Genetics:  
A/Gene: gadd45  
A/Introns: 15/2; 49/2; 128/3



1 MTLLEEVGODTPESTARMOGAGKALHELLLSAOROGCLTAGYVESAKVLNVPDNTVFC 60  
 1 MTLLEESSAAE---QKIERMDVTVDALVEVLKSKARSGRTITGVGEAAKLINVPDNTVLC 57  
 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIIV-----GAGEBA 111  
 58 LLAADDEDDVALQIHFTLIQAFCCENDINILRVSNPGLRIELLLLENDKSPAESGGALA 117  
 112 GAGDHLITLISNPEDAWKDPALFKLSLFCESRSVNDVPSITLPE 159  
 118 QTP-DLHCVLVTNPSSQWQDPALSLICFCRESRYMDQWVPYINLPE 164  
 3 protein - mouse  
 8 Mus musculus (house mouse)  
 e: 03-Feb-1993 #sequence\_revision 03-Feb-1993 #text\_change 09-Jul-2004  
 session: A43813  
 collabl, A.; Lord, K.A.; Hoffman-Liebermann, B.; Liebermann, D.A.  
 Gene 6, 165-167, 1991  
 le: Sequence and expression of a cDNA encoding MyD118: a novel myeloid differentiat  
 erence number: A43813; MUID:9115587L; PMID:1899477  
 session: A43813  
 tus: Preliminary  
 ecule type: mRNA  
 idues: 1-160 <ABD>  
 es-references: UNIPROT:P22339; UNIPARC:UPI000002133B5; GB:X54149; NID:G53290; PIDN:C  
 words: human DNA-damage-inducible protein gadd45  
 verfamily: phosphoprotein

Query Match 52.8%; Score 436; DB 2; Length 160;  
 Local Similarity 53.7%; Pred. No. 1.3e-34;  
 ches 88; Conservative 28; Mismatches 38; Indels 10; Gaps 3;

1 MTLLEEVGODTPESTARMOGAGKALHELLLSAOROGCLTAGYVESAKVLNVPDNTVFC 60  
 1 MTLLEELVASD---NAVQKQAVTAQVQLVAAGQORQLTVGVYEAAKLINVPDNTVLC 57  
 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIIVGAGEEAGF----- 115  
 58 LLAIDDEEEDDIALQIHFTLIQAFCCENDIDIVRGSGMQLAQLL--GEPAETLTGTTEAR 115  
 116 DLHCLILSNPVEDAWKDPALFKLSLFCESRSVNDVPSITLPE 159  
 116 DLHCLILVTNPCHTDSKQGLVEVAVSYCESKGNQWVPYISLEE 159

9 small protein S12 - pig  
 es: Sus scrofa domestica (domestic pig)  
 e: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
 session: J04159; S57497  
 h, O.R.F.; Bauer, H.C.; Richter, K.; Webersinke, G.; Bauer, H.  
 159, 277-278, 1995  
 le: Sequence of the porcine full-length cDNA encoding ribosomal protein rps12.  
 erence number: J04159; MUID:95347612; PMID:7622064  
 session: J04159  
 ecule type: mRNA  
 idues: 1-132 <ZAC>  
 es-references: UNIPROT:P46405; UNIPARC:UPI000000096F; EMBL:X79417; NID:G872314; PID  
 verfamily: rat ribosomal protein S12  
 words: protein biosynthesis; ribosome  
 ry Match 12.5%; Score 103.5; DB 1; Length 132;  
 Local Similarity 25.4%; Pred. No. 0.0097;  
 ches 30; Conservative 29; Mismatches 46; Indels 13; Gaps 4;

Query 25 ALHELLLSAOROGCLTAGYVESAKVLNVPDNTVFCVLAAGEDEBDIALQIHFTLIQAF 84  
 Db 17 ALQEVLTALIHDLARGIREAKAL--DKRAHLCTLVLSNCE-----PMYKLVLEAL 68  
 85 CCENDIDIVRGDVORLAIIVAG--EEAGAPDL--HCILISNPEDAWKDPALFK 137  
 Db 69 CAHQINILKVDNKKLGEMVGLCKIDREGKPRKRVGSCVYKDGKESQAVDIEE 126

RESULT 8

151557  
 ribosomal protein S12 - African clawed frog  
 C/Species: Xenopus laevis (African clawed frog)  
 C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
 C/Accession: 151557  
 R/Seery, L.T.; Schoenberg, D.R.; Canning, M.E.; Whitehead, A.S.  
 Gene 150, 331-333, 1994  
 A/Title: Identification and characterization of a cDNA encoding ribosomal protein S12 f  
 A/Reference number: 151557; MUID:95121924; PMID:7621801  
 A/Accession: 151557  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-132 <SEB>  
 A/Cross-references: UNIPROT:P47840; UNIPARC:UPI00001715BD; GB:L32600; NID:G484042; PIDN  
 C/Superfamily: rat ribosomal protein S12

Query Match 12.3%; Score 101.5; DB 2; Length 132;  
 Best Local Similarity 24.2%; Pred. No. 0.015;  
 Matches 31; Conservative 29; Mismatches 55; Indels 13; Gaps 4;

Query 15 STARMOGAGKALHELLLSAOROGCLTAGYVESAKVLNVPDNTVFCVLAAGEDEBDIAL 74  
 Db 7 SAGVNDVNTALQEVLTALIHDLARGIREAKAL--DKRAHLCTLVLSNCE----- 58  
 75 QIHFTLIQAFCCENDIDIVRGDVORLAIIVAG--EEAGAPDL--HCILISNPEDA 129  
 Db 59 PMYKLVLEALCAEPQINILKVDNKKLGEMVGLCKIDREGKPRKRVGSCVYKDGKES 118  
 Query 130 WKDPALFK 137  
 Db 119 QAKDVIEE 126

RESULT 9

741651  
 40s ribosomal protein S12 - fission yeast (schizosaccharomyces pombe)  
 C/Species: Schizosaccharomyces pombe  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 R/Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, August 1998  
 A/Reference number: Z22007  
 A/Accession: T41651  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-145 <HAR>  
 A/Cross-references: UNIPROT:O14062; UNIPARC:UPI0000132ECE; EMBL:AL031323; PIDN:CAA20436  
 A/Experimental source: strain 972h-; cosmid c962  
 C/Genetics:  
 A/Map position: 3  
 A/Intons: 127/3  
 C/Superfamily: rat ribosomal protein S12

Query Match 12.2%; Score 101; DB 2; Length 145;  
 Best Local Similarity 26.5%; Pred. No. 0.019;  
 Matches 39; Conservative 25; Mismatches 51; Indels 32; Gaps 7;

Query 3 LEEVVGODTPESTARMOGAGKALHELLLSAOROGCLTAGYVESAKVLNVPDNTVFCVL 62  
 Db 14 VEEVEVAAAPETVS---VEDALKEVLKRALVHDGLARGIREASKAL--DRQAHLCTLV 67  
 63 AAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIIVGAGEEAG-----APGDL 117







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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

protein - protein search, using sw model

June 2, 2006, 22:32:55 ; Search time 143 Seconds  
(without alignments)  
1028.514 Million cell updates/sec

US-10-089-641-2

1 MTLLEVRGQDTPVESTARMQ.....LFCESRSVNDVPSITLPE 159

ng table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 2849598

num DB seq length: 0

num DB seq length: 200000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Score	Query	Match Length	ID	Description
826	100.0	159	GA45G_HUMAN	095257 homo sapien
826	100.0	159	05V287_HUMAN	05V287 homo sapien
823	99.6	159	06I166_HUMAN	06I166 homo sapien
814	98.5	159	09U182_HUMAN	09U182 homo sapien
799	96.7	159	09R080_MOUSE	09R080 mus musculu
796	96.4	159	GA45G_RAT	09R080 mus musculu
796	96.4	159	09R080_MOUSE	09R080 mus musculu
794	96.1	159	09R080_MOUSE	09R080 mus musculu
787	95.3	159	GA45G_MOUSE	09R080 mus musculu
737	89.2	141	05V288_HUMAN	05V288 homo sapien
675	81.7	159	02H2D5_CHICK	02H2D5 gallus galli
665	80.9	159	06U0P4_XENLA	06U0P4 xenopus lae
652	78.9	159	06D1D3_XENTR	06D1D3 xenopus tro
651	78.8	159	07X2C4_XENLA	07X2C4 xenopus lae
642	77.7	159	03KPS5_XENLA	03KPS5 xenopus lae
548.5	66.4	159	06P021_BRARE	06P021 brachydanio
543.5	65.8	155	04R1X0_TETNG	04R1X0 tetraodon n
498.5	60.4	155	06N0V6_BRARE	06N0V6 brachydanio
477	57.7	156	06GMM1_BRARE	06GMM1 brachydanio
475	57.5	158	03I9S4_ORYLA	03I9S4 oryzias lat
469.5	56.8	146	04T9H6_TETNG	04T9H6 tetraodon n
465.5	56.4	157	02H2D6_CHICK	02H2D6 gallus galli
463.5	56.1	157	07X2Z4_XENLA	07X2Z4 xenopus lae
462.5	56.0	165	03ZBN6_BOVIN	03ZBN6 bos taurus
457.5	55.4	157	06NYS7_BRARE	06NYS7 brachydanio
457.5	55.4	165	GA45A_HUMAN	P24522 homo sapien
457.5	55.4	165	06O0G15_FELCA	06O0G15 felis silve
451.5	54.7	165	GA45A_MOUSE	P48316 mus musculu

32	451.5	54.7	165	2	03UMH6_MOUSE	03UMH6 mus musculu
33	447	54.1	160	1	GA45B_HUMAN	075293 homo sapien
34	446	54.0	160	2	05E9A5_BOVIN	05E9A5 bos taurus
35	439.5	53.2	165	2	06H1L6_RAT	06H1L6 rattus norv
36	436.5	52.8	165	1	GA45A_RAT	048317 rattus norv
37	436	52.8	160	1	GA45B_MOUSE	P22339 mus musculu
38	436	52.8	160	2	03U342_MOUSE	03U342 m mod-deriv
39	436	52.8	160	2	05U322_RAT	05U322 rattus norv
40	435	52.7	158	2	05N021_BRARE	05N021 brachydanio
41	416.5	50.4	159	2	06P051_BRARE	06P051 brachydanio
42	413	50.0	155	2	04T9E6_TETNG	04T9E6 tetraodon n
43	355	43.0	131	2	05TCA7_HUMAN	05TCA7 homo sapien
44	285	34.5	318	2	04RMR7_TETNG	04RMR7 tetraodon n
45	253	30.6	51	2	05MA13_HUMAN	05MA13 homo sapien

## ALIGNMENTS

RESULT 1  
GA45G\_HUMAN STANDARD; PRT; 159 AA.  
ID GA45G\_HUMAN 095257; 09C076;  
AC 30-MAY-2000 Integrated into UniProtKB/Swiss-Prot.  
DT 01-MAY-1999, sequence version 1.  
DT 07-FEB-2006, entry version 43.  
DE Growth arrest and DNA-damage-inducible protein GADD45 gamma (Cytokine-responsive protein CR6).  
GN Name=GADD45G; Synonyms=CR6;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99043506; PubMed=9827804; DOI=10.1016/S0092-8674(00)81619-0;  
RA Takekawa M., Salto H.,  
RT "A family of stress-inducible GADD45-like proteins mediate activation of the stress-responsive MTK1/MEK4 MAPKK.";  
RL Cell 95:521-530(1998).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20065129; PubMed=10597261; DOI=10.1038/sj.onc.1203054;  
RA Fan W., Richter G., Cereseto A., Beadling C., Smith K.A.,  
RT "Cytokine response gene 6 induces p21 and regulates both cell growth and arrest.";  
RL Oncogene 18:6573-6582(1999).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99043506; PubMed=9827804; DOI=10.1016/S0092-8674(00)81619-0;  
RA Jung N., Yi Y., Kim D., Shong M., Hong S., Lee H., Bae I.,  
RT "Cloning and characterization of Gadd45 gamma gene and its regulation by C/EBP.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE, AND VARIANT SER-112.  
RX MEDLINE=20237539; PubMed=10773677;  
RA Gong R., Yu L., Zhang H., Tu Q., Zhao Y., Yang J., Xu Y., Zhao S.,  
RT "Assignment of human GADD45G to chromosome 9q22.1--q22.3 by radiation hybrid mapping.";  
RL Cytogenet. Cell Genet. 88:95-96(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RA Kainane N., Chen X., Rolfs A., Halliack A., Hines L., Eisenstein S.,  
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,  
RA "Cloning of human full-length cDNAs in BD Creator(TM) system donor vector.";  
RT Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT SER-112.  
RA Rider M.J., Braun A.C., Montoya M.A., Chung M.-W., Nguyen C.P.,  
RA Nguyen D.A., Livingston R.J., Poel C.L., Robertson P.D.,

Schackwitz W.S., Sherwood J.K., Wiltrak L.A., Nickerson D.A.;  
 "NIHES-SNPs, environmental genome project, NIHES ES15478, Department  
 of Genome Sciences, Seattle, WA (URL: <http://esg.gs.washington.edu>).";  
 Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

[7] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

TISSUE=Lung;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schlier G.D.,

Altehusl S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Jopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsien F.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Stapleton M., Uedon T.B., Toshiyuki S., Caminci P., Prange C.,

Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

Josak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- FUNCTION: Involved in the regulation of growth and apoptosis.

-1- Mediates activation of stress-responsive MTK1/MEK4 MAPKKK.

-1- INTERACTION: Q92993:HTATP; NbExp=1; IntAct=EBI-448202, EBI-399080;

Q9P9H0:RIAA1377; NbExp=1; IntAct=EBI-448202, EBI-473176;

Q9Y3C7:MEB1; NbExp=1; IntAct=EBI-448202, EBI-394707;

Q9BVU6:ITP14A; NbExp=1; IntAct=EBI-448202, EBI-473284;

-1- SIMILARITY: Belongs to the GADD45 family.

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EMBL: AF078078; AAC83329.1; -; mRNA.

EMBL: AF079806; AAD28544.1; -; mRNA.

EMBL: AF265659; AAF73468.1; -; Genomic\_DNA.

EMBL: AF087883; AAK0414.1; -; mRNA.

EMBL: BT007234; AAP35898.1; -; mRNA.

EMBL: AF494037; AAM00007.1; -; Genomic\_DNA.

EMBL: BC000465; AAM00465.1; -; mRNA.

EMBL: BC019325; AAI19325.1; -; mRNA.

IntAct: Q9S257; -;

Ensembl: ENSG00000130222; Homo sapiens.

-1-InvDB: HIX008156; -;

IGNC: HGNC:4097; GAD45G.

WIM: 604949; Gene.

30; GO:000515; F:protein binding; IPI

30; GO:000185; P:activation of MAPKK activity; TAS.

30; GO:0006281; P:DNA repair; TAS.

30; GO:0006950; P:response to stress; TAS.

InterPro: IPR004038; Ribosomal L7A.

InterPro: IPR01248; Ribosomal L7Ae; 1.

InterPro: Developmental protein; Polymorphism.

InterPro: Growth arrest and DNA-damage-inducible

protein GADD45 gamma.

/Prid=PRO\_0000148336.

G -> S (in dbSNP:318505).

/FTid=VAR\_01888.

OR -> HG (in Ref. 4).

APG -> CAC (in Ref. 4).

SEQUENCE 159 AA; 17121 MW; 26427ES581941B64 CRC64;

Local Similarity 100.0%; Score 826; DB 1; Length 159;

Local Similarity 100.0%; Pred. No. 3e-71;

Ches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLSEVRGDDTVPESTARNOGAKLHELLLSAOROGCTTAGYESAKYLVNDPDNVTC 60  
 DB 1 MTLSEVRGDDTVPESTARNOGAKLHELLLSAOROGCTTAGYESAKYLVNDPDNVTC 60  
 QY 61 VLAAGEDEBDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIYVAGEBAGAPGDLHCT 120  
 DB 61 VLAAGEDEBDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIYVAGEBAGAPGDLHCT 120  
 QY 121 LISNPEDAMKDPALFKSLFCEESRSVNDWVPSITLPE 159  
 DB 121 LISNPEDAMKDPALFKSLFCEESRSVNDWVPSITLPE 159

#### RESULT 2

05V287 HUMAN PRELIMINARY; PRT; 159 AA.  
 ID 05V287 HUMAN  
 AC 05V287;  
 DT 10-MAY-2005; Integrated into UniProtKB/TrEMBL.  
 DT 10-MAY-2005; sequence version 1.  
 DT 07-FEB-2006; entry version 4.  
 DE Growth arrest and DNA-damage-inducible, gamma.  
 GN Name=GADD45G; ORFNames=RP11-260L6.1-001;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Brown J.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

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 CC -----  
 DR EMBL: AL161910; CAH71791.1; -; Genomic\_DNA.  
 DR Ensembl: ENSG00000130222; Homo sapiens.  
 DR InterPro: IPR004038; Ribosomal L7A.  
 DR Pfam: PF01248; Ribosomal L7Ae; 1.  
 SQ SEQUENCE 159 AA; 17121 MW; 26427ES581941B64 CRC64;

Query Match 100.0%; Score 826; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 3e-71;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLSEVRGDDTVPESTARNOGAKLHELLLSAOROGCTTAGYESAKYLVNDPDNVTC 60  
 DB 1 MTLSEVRGDDTVPESTARNOGAKLHELLLSAOROGCTTAGYESAKYLVNDPDNVTC 60  
 QY 61 VLAAGEDEBDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIYVAGEBAGAPGDLHCT 120  
 DB 61 VLAAGEDEBDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIYVAGEBAGAPGDLHCT 120  
 QY 121 LISNPEDAMKDPALFKSLFCEESRSVNDWVPSITLPE 159  
 DB 121 LISNPEDAMKDPALFKSLFCEESRSVNDWVPSITLPE 159

#### RESULT 3

061AM6 HUMAN PRELIMINARY; PRT; 159 AA.  
 ID 061AM6 HUMAN  
 AC 061AM6;  
 DT 05-JUL-2004; Integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004; sequence version 1.  
 DT 07-FEB-2006; entry version 7.  
 DE GADD45G protein.  
 GN Name=GADD45G; (Human).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

NUCLEOTIDE SEQUENCE.  
Bbert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;  
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

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Distributed under the Creative Commons Attribution-NonDerivs License

EMBL: CR57038; CAG3319.1; -; mRNA.  
Ensembl: ENSG00000130222; Homo sapiens.  
InterPro: IPR004038; Ribosomal\_L7A.  
Pfam: PF01248; Ribosomal\_L7Ae; 1.  
SEQUENCE 159 AA; 17107 MW; 27F27E581941B64 CRC64;

159.6%; Score 823; DB 2; Length 159;  
Local Similarity 99.4%; Pred. No. 5.9e-71;  
Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MTEEVAGQDTPVSTARMQAGKALHELLLSAQRQGLTAGYVESAKVLNVDPNVTF 60  
1 MTEEVAGQDTPVSTARMQAGKALHELLLSAQRQGLTAGYVESAKVLNVDPNVTF 60  
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVORLAIVGAGEGAGPGLH 120  
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVORLAIVGAGEGAGPGLH 120  
121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159  
121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159

1 4  
2 HUMAN  
GUS2\_HUMAN PRELIMINARY; PRT; 159 AA.  
GUS2;  
01-MAY-2000, integrated into UniProtKB/TrEMBL.  
01-MAY-2000, sequence version 1.  
07-FEB-2006, entry version 16.  
Gadd45-related protein.

Name:GRI7;  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
Homo.  
NCBI\_TaxID=9606;  
[1]

NUCLEOTIDE SEQUENCE.

EMBL: D83023; BAA84543.1; -; mRNA.  
Ensembl: ENSG00000130222; Homo sapiens.  
InterPro: IPR004038; Ribosomal\_L7A.  
Pfam: PF01248; Ribosomal\_L7Ae; 1.  
SEQUENCE 159 AA; 17031 MW; 2642623FB8EA3BD CRC64;

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EMBL: D83023; BAA84543.1; -; mRNA.  
Ensembl: ENSG00000130222; Homo sapiens.  
InterPro: IPR004038; Ribosomal\_L7A.  
Pfam: PF01248; Ribosomal\_L7Ae; 1.  
SEQUENCE 159 AA; 17031 MW; 2642623FB8EA3BD CRC64;

159.5%; Score 814; DB 2; Length 159;  
Local Similarity 98.7%; Pred. No. 4.3e-70;  
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MTEEVAGQDTPVSTARMQAGKALHELLLSAQRQGLTAGYVESAKVLNVDPNVTF 60  
1 MTEEVAGQDTPVSTARMQAGKALHELLLSAQRQGLTAGYVESAKVLNVDPNVTF 60  
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVORLAIVGAGEGAGPGLH 120  
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVORLAIVGAGEGAGPGLH 120

Db 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVORLAIVGAGEGAGPGLH 120  
Qy 121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159  
121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159

RESULT 5  
Q9R0S0\_MOUSE PRELIMINARY; PRT; 159 AA.  
Q9R0S0\_MOUSE  
AC Q9R0S0;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 07-FEB-2006, entry version 18.  
DE OIG37 (GADD45G).  
GN Name=Gadd45g; Synonyms=oig37;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
[1]  
1] NUCLEOTIDE SEQUENCE.  
RX MEDLINE=99386956; PubMed=10455148; DOI=10.1074/jbc.274.35.24766;  
RA Nakayama K., Hara T., Hibi M., Hirano T., Miyajima A.;  
RT "A novel oncogene M-inducible gene OIG37 forms a gene family with  
J. Biol. Chem. 274:24766-24772(1999).  
[2]

NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SV;  
RA Bailliet A.G., Hollander M.C., Fornace A.J. Jr., Hoffman B.,  
RA Liebermann D.A.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

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EMBL: AB021884; BAA78538.1; -; mRNA.  
EMBL: AY258502; AAF79506.1; -; Genomic DNA.  
DR Ensembl: ENSMUSG00000021453; Mus musculus.  
DR MGI: 1346325; Gadd45g.  
DR GO: 0005634; C:nucleus; TAS.  
DR GO: 0005515; F:protein binding; IPI.  
DR GO: 0000186; P:activation of MAPK activity; IDA.  
DR GO: 0042095; P:interferon-gamma biosynthesis; TAS.  
DR GO: 0006469; P:negative regulation of protein kinase activity; IDA.  
DR GO: 0000074; P:regulation of progression through cell cycle; IDA.  
DR GO: 0045063; P:helper 1 cell differentiation; TAS.  
DR InterPro: IPR004038; Ribosomal\_L7A.  
DR Pfam: PF01248; Ribosomal\_L7Ae; 1.  
SEQUENCE 159 AA; 17301 MW; 4B598AF54529BD96 CRC64;

Query Match 96.7%; Score 799; DB 2; Length 159;  
Best Local Similarity 96.9%; Pred. No. 1.2e-68;  
Matches 154; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 MTEEVAGQDTPVSTARMQAGKALHELLLSAQRQGLTAGYVESAKVLNVDPNVTF 60  
1 MTEEVAGQDTPVSTARMQAGKALHELLLSAQRQGLTAGYVESAKVLNVDPNVTF 60  
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVORLAIVGAGEGAGPGLH 120  
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVORLAIVGAGEGAGPGLH 120  
121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159  
121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159

RESULT 6  
GA45G\_RAT STANDARD; PRT; 159 AA.  
ID GA45G\_RAT

29WT07;  
30-MAY-2000, integrated into UniProtKB/Swiss-Prot.  
31-NOV-1999, sequence version 1.  
37-FEB-2006, entry version 22.  
Growth arrest and DNA-damage-inducible protein GADD45 gamma.  
Name:Gadd45g;  
Rattus norvegicus (Rat).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
Muridae; Muridae; Murinae; Rattus.  
NCBI\_Taxid=10116;  
[1]  
Nucleotide sequence [MRA].  
MEDLINE=99198964; PubMed=10100865; DOI=10.1016/S0014-5793(99)00234-3;  
Kojima S., Mayumi-Matsuda K., Suzuki H., Sakata T.;  
"Molecular cloning of rat GADD45gamma, gene induction and its role  
during neuronal cell death";  
FEBS Lett. 446:313-317(1999).  
-1- FUNCTION: Involved in the regulation of growth and apoptosis.  
Mediates activation of stress-responsive MTK1/MEKKA MAPKK.  
-1- SIMILARITY: Belongs to the GADD45 family.  
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distributed under the Creative Commons Attribution-NonDerivs license  
EMBL; AB020978; BAA78094.1; -; mRNA.  
Ensembl; ENSRNOG0000013090; Rattus norvegicus.  
GDD; 1311796; Gadd45g.  
InterPro; IPR004038; Ribosomal L7A.  
Pfam; PF01248; Ribosomal L7ae; 1.  
Apoptosis; Developmental protein; Differentiation;  
protein arrest and DNA-damage-inducible  
HAIN 1 159  
SEQUENCE 159 AA; 17287 MW; 4B598B339E45C96 CRC64;  
CY Match 96.4%; Score 796; DB 1; Length 159;  
- Local Similarity 96.2%; Pred. No. 2.3e-68;  
- Cons 153; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
1 MTLSEVRGQDTPESTARMQAGKALHLLLSAQRQGLTAGYVESAKVLNVPDVTFC 60  
1 MTLSEVRGQDTPESTARMQAGKALHLLLSAQRQGLTAGYVESAKVLNVPDVTFC 60  
61 VLAAGEDEGDIALQIFHTLIQAFCCENDIDIVRGDVORLAIIVAGBEGAPGDLHCI 120  
61 VLAAGEDEGDIALQIFHTLIQAFCCENDIDIVRGDVORLAIIVAGBEGAPGDLHCI 120  
121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159  
121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159  
3 MOUSE PRELIMINARY; PRT; 159 AA.  
399M58;  
31-JUN-2001, integrated into UniProtKB/TrEMBL.  
37-FEB-2006, entry version 17.  
Growth arrest and DNA-damage-inducible 45 gamma.  
Name=Gadd45g;  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
Muridae; Muridae; Murinae; Mus.  
NCBI\_Taxid=10090;  
[1]  
Nucleotide sequence.  
STRAIN=CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor  
arose spontaneously;  
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
Straussberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahney J., Helton E., Kettelman M., Madan A., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
Nucleotide sequence.  
STRAIN=CZECH II; TISSUE=Mammary tumor metastasized to lung. Tumor  
arose spontaneously;  
Straussberg R.;  
Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
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EMBL; BC001989; AAH01989.1; -; mRNA.  
Ensembl; ENSMUSG0000021453; Mus musculus.  
DR MGI; MGI:1346325; Gadd45g.  
DR GO; GO:0005634; C:nucleus; TAS.  
DR GO; GO:0005515; F:protein binding; IPT.  
DR GO; GO:0000186; P:activation of MAPK activity; IDA.  
DR GO; GO:0042095; P:interferon-gamma biosynthesis; TAS.  
DR GO; GO:0006469; P:negative regulation of protein kinase activity; IDA.  
DR GO; GO:0000774; P:regulation of progression through cell cycle; IDA.  
DR GO; GO:0045063; P:regulation of cell differentiation; TAS.  
DR InterPro; IPR004038; Ribosomal L7A.  
DR Pfam; PF01248; Ribosomal L7ae; 1.  
DR SEQUENCE 159 AA; 17317 MW; C9598AF5AC9BD89 CRC64;  
Query Match 96.4%; Score 796; DB 2; Length 159;  
Best Local Similarity 96.2%; Pred. No. 2.3e-68;  
Matches 153; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 MTLSEVRGQDTPESTARMQAGKALHLLLSAQRQGLTAGYVESAKVLNVPDVTFC 60  
QY 1 MTLSEVRGQDTPESTARMQAGKALHLLLSAQRQGLTAGYVESAKVLNVPDVTFC 60  
DB 1 MTLSEVRGQDTPESTARMQAGKALHLLLSAQRQGLTAGYVESAKVLNVPDVTFC 60  
DB 1 MTLSEVRGQDTPESTARMQAGKALHLLLSAQRQGLTAGYVESAKVLNVPDVTFC 60  
QY 61 VLAAGEDEGDIALQIFHTLIQAFCCENDIDIVRGDVORLAIIVAGBEGAPGDLHCI 120  
QY 61 VLAAGEDEGDIALQIFHTLIQAFCCENDIDIVRGDVORLAIIVAGBEGAPGDLHCI 120  
DB 61 VLAAGEDEGDIALQIFHTLIQAFCCENDIDIVRGDVORLAIIVAGBEGAPGDLHCI 120  
QY 121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159  
QY 121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159  
DB 121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159  
RESULT 8  
Q2KX1 BOVIN  
ID Q2KX1 BOVIN PRELIMINARY; PRT; 159 AA.  
AC Q2KX1;  
DT 07-MAR-2006, integrated into UniProtKB/TrEMBL.  
DT 07-MAR-2006, sequence version 1.  
DT 07-MAR-2006, entry version 1.  
DE Hypothetical protein.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
OC Pecora; Bovidae; Bovinae; Bos.  
NCBI\_Taxid=9913;



25V268 HUMMAN PRELIMINARY; PRT; 141 AA.  
25V268;  
07-DEC-2004, integrated into UniProtKB/TrEMBL.  
07-DEC-2004, sequence version 1.  
07-FEB-2006, entry version 8.  
Growth arrest and DNA-damage-inducible, gamma.  
Name=GADD45G; ORFNames=RP11-260L6.1-002;  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;  
NCBI\_TaxId=9606;  
[1]  
NUCLEOTIDE SEQUENCE.  
Brown T.;  
Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.

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EMBL; AL161910; CAH71790.1; -; Genomic DNA.  
Ensembl; ENSG00000130222; Homo sapiens.  
InterPro: IPR004038, Ribosomal L7A.  
Pfam; PF01248; Ribosomal L7Ae; 1.  
SEQUENCE 141 AA; 15120 MW; 073B15AC5D4D5818 CRC64;

-----  
CY Match 89.2%; Score 737; DB 2; Length 141;  
Local Similarity 100.0%; Pred. No. 9.7e-63;  
Res 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 MGAGAGALHELLISAROGCTTAGYVESAKVLPNDPNTFCVLAAGEDESDIALQTHF 78  
1 MGAGAGALHELLISAROGCTTAGYVESAKVLPNDPNTFCVLAAGEDESDIALQTHF 60  
79 TLIOAFCCNDNDIYVGVORLAIVAGEEAGAPGDLHTLISNPEDAKWDALKEKL 138  
61 TLIOAFCCNDNDIYVGVORLAIVAGEEAGAPGDLHTLISNPEDAKWDALKEKL 120  
139 SLFCEESRSVNDWVPSITLPE 159  
121 SLFCEESRSVNDWVPSITLPE 141

F 11  
5 CHICK  
22H2D5\_CHICK PRELIMINARY; PRT; 159 AA.  
22H2D5;  
07-MAR-2006, integrated into UniProtKB/TrEMBL.  
07-MAR-2006, sequence version 1.  
07-MAR-2006, entry version 1.  
Growth arrest and DNA-damage-inducible protein 45 gamma.  
Name=gadd45;  
Gallus gallus (Chicken).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
Gallus.  
NCBI\_TaxId=9031;  
[1]  
NUCLEOTIDE SEQUENCE.  
Wang Y., Li J., Leung F.C.;  
"Expression and Regulation of Growth Arrest and DNA-damage-inducible  
Protein GADD45 in the Chicken Ovary."  
Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.

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EMBL; DQ358722; ABC88380.1; -; mRNA.  
SEQUENCE 159 AA; 17411 MW; 97751B75087626F CRC64;

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CY Match 81.7%; Score 675; DB 2; Length 159;  
Local Similarity 78.0%; Pred. No. 1e-56;  
Res 144; Conservative 18; Mismatches 17; Indels 0; Gaps 0;

QY MLEEVYRGDDVPESNARHQAGKALHETLLLSAOROGCLTGVYESAKLVANVPDNPVFC 60  
 Db 1 MTLLEETVQGGEPVPACKDMQMGAGKALHETLLLSAOROGCLTGVYESAKLVANVPDNPVAF 60  
 QY VLAAGEBEDGDIALQIHFTLLIOAFCCENDIDIVRGDVQRIALAVGAGEAGAPGDHCT 120  
 Db 61 VLAABEDBDGDIALQIHFTLLIOAFCCENDIDIVRSLDPLKLAALGSGEESGEPDRDHCT 120  
 QY 121 LISNPEDAMKOPALEKLSLPEEERSNVDPVPSITLPE 159  
 Db 121 LITPNEDGMKOPSLKLNCFCEERSNINEMVPTIALPE 159  
 RESULT 12  
 Qe0UP4\_XENLA PRELIMINARY; PRT: 159 AA.  
 AC Qe0UP4;  
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2002, sequence version 1.  
 DT 07-FEB-2006, entry version 14.  
 DE XGadd45-gamma protein.  
 GN Name:XGadd45-gamma;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 CC Xenopodinae; Xenopus; Xenopus.  
 OX NCBI\_TaxId=8355;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA MEDLINE=22274402; PubMed=12385755; DOI=10.1016/S0925-4773(02)00296-4;  
 RX De la Calle-Mustienes E., Glavic A., Modolell J., Gomez-Skarmeta J.;  
 RT "Xlro homeoproteins coordinate cell cycle exit and primary neuron  
 RT formation by upregulating neuronal fate repressors and downregulating  
 RT the cell-cycle inhibitor XGadd45-gamma";  
 RL Mech. Dev. 119:69-80(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Gomez-Skarmeta J.L.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT initiative";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Whole;  
 RX MEDLINE=23868257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Peingold E.A., Grout L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuller G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Ditschenko L., Marzinska K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udén T.B., Teshiyuki S., Carinini P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McEhernan K.U., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.W.,  
 RA Villalón D.K., Muzny D.M., Gregorenko E.J., Lu X., Gibbs R.A.,  
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Binkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
 RA Rikkesley A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalium D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).



[5]  
NUCLEOTIDE SEQUENCE.

TISSUE=Whole;

Klein S., Gerhard D.S.;  
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

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EMBL: AJ414384; CAC88862.1; -; mRNA.

EMBL: BC078567; AAH78567.1; -; mRNA.

InterPro: IPR004038; Ribosomal\_L7A.

Pfam: PF01248; Ribosomal\_L7Ae; 1.

SEQUENCE 159 AA; 17828 MW; E8A9264B12C1771B CRC64;

Query Match 80.5%; Score 665; DB 2; Length 159;

Local Similarity 78.0%; Pred. No. 9.6e-56; Mismatches 18; Indels 0; Gaps 0;

Ches 124; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

1 MTLSEVRGQDTPVESTARMQAGKALHELLLSAQRQCLTAGYESAKVLNVPDNTFC 60

1 MTLSEVHGQETVESADRMQAGKALHELLLSAQRQCLTAGYESAKVLNVPDNTFC 60

61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDYRVGDVQRLAIVAGGEAGAPGDLHCI 120

61 ILAADYDEGDIALQIHFTLIQAFCCENDIDYRVGDVQRLAIVAGGEAGAPGDLHCI 120

121 LISNPEDAMKDPALKELSLFCESRSVNDVPSITLPE 159

121 LITNPEDAMKDPALKELSLFCESRSVNDVPSITLPE 159

3 XENTR PRELIMINARY; PRT; 159 AA.

3 XENTR PRELIMINARY; PRT; 159 AA.

16-AUG-2004, integrated into UniProtKB/TrEMBL.

16-FEB-2006, entry version 10.

MGC89481 protein.

Name=MGC89481;

Xenopus tropicalis (Western clawed frog) (Silurana tropicalis);

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus; Silurana.

NCBI\_TaxID=8364;

NCBI\_TaxID=8364;

NCBI\_TaxID=8364;

NCBI\_TaxID=8364;

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NCBI\_TaxID=8364;

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NCBI\_TaxID=8364;

NCBI\_TaxID=8364;

RA Klein S., Gerhard D.S.;

Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

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EMBL: BC075545; AAH75545.1; -; mRNA.

InterPro: IPR004038; Ribosomal\_L7A.

Pfam: PF01248; Ribosomal\_L7Ae; 1.

SEQUENCE 159 AA; 17754 MW; 70F9C42998FEA814 CRC64;

Query Match 78.9%; Score 652; DB 2; Length 159;

Best Local Similarity 76.7%; Pred. No. 1.7e-54;

Matches 122; Conservative 17; Mismatches 20; Indels 0; Gaps 0;

1 MTLSEVRGQDTPVESTARMQAGKALHELLLSAQRQCLTAGYESAKVLNVPDNTFC 60

1 MTLSEVHGQETVESADRMQAGKALHELLLSAQRQCLTAGYESAKVLNVPDNTFC 60

61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDYRVGDVQRLAIVAGGEAGAPGDLHCI 120

61 ILAADYDEGDIALQIHFTLIQAFCCENDIDYRVGDVQRLAIVAGGEAGAPGDLHCI 120

121 LISNPEDAMKDPALKELSLFCESRSVNDVPSITLPE 159

121 LITNPEDAMKDPALKELSLFCESRSVNDVPSITLPE 159

3 XENTR PRELIMINARY; PRT; 159 AA.

3 XENTR PRELIMINARY; PRT; 159 AA.

16-AUG-2003, integrated into UniProtKB/TrEMBL.

01-JUN-2003, sequence version 1.

07-FEB-2006, entry version 11.

MGC53682 protein.

Name=MGC53682;

Xenopus laevis (African clawed frog);

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus; Xenopus.

NCBI\_TaxID=8355;

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NCBI\_TaxID=8355;

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NCBI\_TaxID=8355;

NCBI\_TaxID=8355;

NCBI\_TaxID=8355;

NCBI\_TaxID=8355;

NCBI\_TaxID=8355;

Dev. Dyn. 225:384-391(2002).  
 [3]  
 NUCLEOTIDE SEQUENCE.  
 TISSUE=Embryo;  
 Klein S., Strausberg R.,  
 Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
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 3MBL; BC045055; AAH45055.1; -; mRNA.  
 InterPro: IPR004038; Ribosomal\_L7A.  
 Pfam: PF01248; Ribosomal\_L7Ae; 1.  
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 Y Match 78.8%; Score 651; DB 2; Length 159;  
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 Cons 122; Conservative 17; Mismatches 20; Indels 0; Gaps 0;  
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 61 VIAAGEDEGDIALQIHFTLQAFCCENDIDIVRGVORLAIYVAGEGAGAPGDLH 120  
 61 ILAADYDEGDIALQIHFTLQAFCCENDINIVRLNDEKVAQILGFTDESAPKDLH 120  
 121 LITNPEDAMKDPALKEKLSLFCESRSVNDWVPSITLPE 159  
 121 LITNPEDAMKDPALKEKLSLFCESRSVNDWVPSITLPE 159  
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 15  
 3 XENLA PRELIMINARY; PRT; 159 AA.  
 3KPP5,  
 38-NOV-2005, integrated into UniProtKB/TrEMBL.  
 38-NOV-2005, sequence version 1.  
 37-FEB-2006, entry version 4.  
 MGCS3682 protein.  
 Name=MGCS3682;  
 Xenopus laevis (African clawed frog).  
 Chordata; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;  
 Xenopodinae; Xenopus; Xenopus.  
 NCBI\_TaxID=8355;  
 [1]  
 NUCLEOTIDE SEQUENCE.  
 TISSUE=Brain;  
 EDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 Topkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 Jatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
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 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huily S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.,  
 Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
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 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,  
 RA Schermer A., Schein J.E., Jones S.J.W., Maira M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RA Klein S., Gerhard D.S.,  
 RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.  
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms  
 CC Distributed under the Creative Commons Attribution-NonDerivs license  
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 CC EMBL; BC106626; AA106627.1; -; mRNA.  
 DR InterPro: IPR004038; Ribosomal\_L7A.  
 DR Pfam: PF01248; Ribosomal\_L7Ae; 1.  
 SO SEQUENCE 159 AA; 1771 MW; 7E2527FAD0884374 CRC64;  
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 Query Match 77.7%; Score 642; DB 2; Length 159;  
 Best Local Similarity 76.1%; Pred. No. 1.6e-53;  
 Matches 121; Conservative 17; Mismatches 21; Indels 0; Gaps 0;  
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 Db 1 MTLSEVVGQDTVPESADRMQAGKALHELLLSAQRQGLTAGYVESAKVLPDNDVTF 60  
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 Db 61 ILAADYDEGDIALQIHFTLQAFCCENDINIVRLNDEKVAQILGFTDESAPKDLH 120  
 QY 121 LITNPEDAMKDPALKEKLSLFCESRSVNDWVPSITLPE 159  
 Db 121 LITNPEDAMKDPALKEKLSLFCESRSVNDWVPSITLPE 159  
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 Search completed: June 2, 2006, 22:36:46  
 Job time : 147 secs

GenCore version 5.1.9  
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Protein - protein search, using sw model

June 2, 2006, 22:37:00 ; Search time 27 Seconds  
(without alignments)  
515.458 Million cell updates/sec

US-10-089-641-2  
1 MLEEVYRGQDTVPSTARMQ.....LFCESRSVNDWPSITLPE 159

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Gapop 10.0 , Gapext 0.5

650591 seqs, 87530628 residues

number of hits satisfying chosen parameters: 650591

um DB seq length: 0  
um DB seq length: 200000000

rocessing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Issued Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/prodata/2/1aa/5-COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/1aa/6-COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/1aa/7-COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/1aa/H-COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/1aa/RE-COMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/1aa/BACKFILE1.pep:\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/1aa/BACKFILE1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Score	Query Match	Length	ID	Description
826	100.0	159	1 US-08-463-081B-12	Sequence 12, Appl
826	100.0	159	1 US-08-461-379A-12	Sequence 12, Appl
826	100.0	159	1 US-08-462-390B-12	Sequence 12, Appl
826	100.0	159	2 US-08-463-074B-12	Sequence 12, Appl
826	100.0	159	2 US-08-465-585C-12	Sequence 12, Appl
826	100.0	159	2 US-08-652-446-12	Sequence 12, Appl
826	100.0	159	2 US-09-534-811-7	Sequence 7, Appl
826	100.0	159	3 US-10-600-158-7	Sequence 7, Appl
826	100.0	159	3 US-09-949-016-9744	Sequence 9744, Ap
814	98.5	159	1 US-08-797-831A-1	Sequence 1, Appl
814	98.2	160	2 US-09-879-833-2	Sequence 2, Appl
457.5	55.4	165	1 US-08-602-208-3	Sequence 3, Appl
457.5	55.4	165	2 US-09-534-811-2	Sequence 2, Appl
457.5	55.4	165	2 US-05-208-206-3	Sequence 3, Appl
457.5	55.4	165	3 US-10-600-158-2	Sequence 2, Appl
451.5	54.7	165	3 US-09-534-811-8	Sequence 8, Appl
451.5	54.7	165	3 US-10-600-158-8	Sequence 8, Appl
447	54.1	160	2 US-09-534-811-6	Sequence 6, Appl
447	54.1	160	2 US-10-600-158-6	Sequence 6, Appl
445	53.9	192	2 US-09-949-016-7665	Sequence 7665, Ap
436.5	52.8	165	2 US-09-534-811-9	Sequence 9, Appl
436.5	52.8	165	3 US-10-600-158-9	Sequence 9, Appl
436	52.8	160	1 US-08-602-208-4	Sequence 4, Appl
436	52.8	160	2 US-08-602-208-2	Sequence 2, Appl
422	51.1	160	2 US-09-208-206-4	Sequence 2, Appl
422	51.1	160	2 US-09-208-206-2	Sequence 2, Appl

27	200	24.2	46	2	US-09-534-811-16	Sequence 16, Appl
28	200	24.2	46	3	US-10-600-158-16	Sequence 16, Appl
29	184	22.3	41	2	US-09-534-811-32	Sequence 32, Appl
30	184	22.3	41	3	US-10-600-158-32	Sequence 32, Appl
31	164	19.9	38	2	US-09-534-811-17	Sequence 17, Appl
32	164	19.9	38	3	US-10-600-158-17	Sequence 17, Appl
33	157	19.0	36	2	US-09-534-811-31	Sequence 31, Appl
34	157	19.0	36	3	US-10-600-158-31	Sequence 31, Appl
35	146.5	17.7	57	2	US-09-513-999C-6287	Sequence 6287, Ap
36	143	17.3	34	2	US-09-534-811-10	Sequence 10, Appl
37	143	17.3	34	3	US-10-600-158-10	Sequence 10, Appl
38	126	15.3	34	2	US-09-534-811-11	Sequence 11, Appl
39	126	15.3	34	3	US-10-600-158-11	Sequence 11, Appl
40	123	14.9	27	2	US-09-534-811-23	Sequence 23, Appl
41	123	14.9	27	3	US-10-600-158-23	Sequence 23, Appl
42	120	14.5	26	2	US-09-534-811-22	Sequence 22, Appl
43	120	14.5	26	3	US-10-600-158-22	Sequence 22, Appl
44	104	12.6	34	2	US-09-534-811-12	Sequence 12, Appl
45	104	12.6	34	3	US-10-600-158-12	Sequence 12, Appl

## ALIGNMENTS

RESULT 1  
US-08-463-081B-12  
Sequence 12, Application US/08463081B  
Patent No. 5871960  
Patent No. 5871960 5837487  
GENERAL INFORMATION:  
APPLICANT: Smith, Kendall A. & Beadling, Carol  
TITLE OF INVENTION: Nucleic Acids Encoding CRS Polypeptide,  
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
STREET: 444 South Flower St. - Suite 1900  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,081B  
FILING DATE: 5-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/104,736  
FILING DATE: 10-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/796,066  
FILING DATE: 20-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Viviana Anzel, Ph. D.  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 622-7700  
TELEFAX: (213) 489-4210  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 159 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-081B-12  
Query Match 100.0%; Score 826; DB 1; Length 159;  
Best Local Similarity 100.0%; Pred. No. 6.8e-93;

ches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLSEVRGQDTPVESTARMQAGAKALHELLLSAORQGCCTAGYVESAKYLVNDPNDVTF 60  
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61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIVAGEBAGAPGDLHCT 120  
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIVAGEBAGAPGDLHCT 120

121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

1 2  
-461-379A-12  
Sequence 12, Application US/08461379A  
Patent No. 5871961  
GENERAL INFORMATION:  
APPLICANT: Smith, Kendall A. & Beadling, Carol  
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,  
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and  
TITLE OF INVENTION: Expression Thereof  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
CITY: Valley Forge  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19482

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,379A  
FILING DATE: 5-JUNE-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/330,108; 08/104,736  
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Viviana Amzel, Ph. D.  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: DART-070  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610)470-0700  
TELEFAX: (610)470-0701  
FORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 159 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
-461-379A-12

ry Match 100.0%; Score 826; DB 1; Length 159;  
t Local Similarity 100.0%; Pred. No. 6.8e-93;  
ches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLSEVRGQDTPVESTARMQAGAKALHELLLSAORQGCCTAGYVESAKYLVNDPNDVTF 60  
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61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIVAGEBAGAPGDLHCT 120  
61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIVAGEBAGAPGDLHCT 120

121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

Db 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

RESULT 3  
US-08-462-390B-12  
Sequence 12, Application US/08462390B  
Patent No. 5882894  
GENERAL INFORMATION:  
APPLICANT: Smith, K. A., & Beadling, C.  
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and  
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ratner & Prestia  
CITY: Valley Forge  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19482

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,390B  
FILING DATE: 5-JUNE-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/330,108  
FILING DATE: 27-OCT-1994  
APPLICATION NUMBER: USSN 08/104,736  
FILING DATE: 10-AUG-1993  
APPLICATION NUMBER: USSN 07/796,066  
FILING DATE: 20-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Viviana Amzel, Ph. D.  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: DART-040  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610)407-0701  
TELEFAX: (610)407-0700  
FORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 159 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-462-390B-12

Query Match 100.0%; Score 826; DB 1; Length 159;  
Best Local Similarity 100.0%; Pred. No. 6.8e-93;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTLSEVRGQDTPVESTARMQAGAKALHELLLSAORQGCCTAGYVESAKYLVNDPNDVTF 60  
DB 1 MTLSEVRGQDTPVESTARMQAGAKALHELLLSAORQGCCTAGYVESAKYLVNDPNDVTF 60

QY 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIVAGEBAGAPGDLHCT 120  
DB 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGDVORLAIVAGEBAGAPGDLHCT 120

QY 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
DB 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

RESULT 4  
US-08-463-074B-12  
Sequence 12, Application US/08463074B  
Patent No. 6020155  
GENERAL INFORMATION:  
APPLICANT: Smith, Kendall A. & Beadling, Carol

TITLE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector and  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
 ADDRESS: (B) STREET: 444 South Flower St. - Suite 1900  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 900071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0,  
 SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/463,074B  
 FILING DATE: 5-JUN-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/104,736  
 FILING DATE: 10-AUG-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 07/796,066  
 FILING DATE: 20-NOV-91

ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 622-7700  
 TELEFAX: (213) 489-4210

INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 159 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 1-463-074B-12

Query Match 100.0%; Score 826; DB 2; Length 159;  
 Local Similarity 100.0%; Pred. No. 6.8e-93;  
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLSEVVGQDTPVESTARMGAGKALHELLLSAQROGCLTAGYESAKVLNVPDNTFC 60  
 1 MTLSEVVGQDTPVESTARMGAGKALHELLLSAQROGCLTAGYESAKVLNVPDNTFC 60  
 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVQRLAIVGAGEAGAGDILHCI 120  
 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVQRLAIVGAGEAGAGDILHCI 120  
 121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159  
 121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159

US-08-585C-12  
 Sequence 12, Application US/08465585C  
 Patent No. 6027914

GENERAL INFORMATION:  
 APPLICANT: Smith, K. A., & Beadling, C.  
 TITLE OF INVENTION: Nucleic Acids Encoding CRE Polypeptide, Vector  
 TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof  
 NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
 ADDRESS: (B) STREET: 444South Flower St. - Suite 190  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 900071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0,  
 SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/652,446  
 FILING DATE:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/465,585C  
 FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: USSN 08/330,108  
 FILING DATE: 27-OCT-1994  
 APPLICATION NUMBER: USSN 08/104,736  
 FILING DATE: 10-AUG-1993  
 APPLICATION NUMBER: USSN 07/796,066  
 FILING DATE: 20-NOV-1991

ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 622-7700  
 TELEFAX: (213) 4894210

INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 159 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-465-585C-12

Query Match 100.0%; Score 826; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-93;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLSEVVGQDTPVESTARMGAGKALHELLLSAQROGCLTAGYESAKVLNVPDNTFC 60  
 1 MTLSEVVGQDTPVESTARMGAGKALHELLLSAQROGCLTAGYESAKVLNVPDNTFC 60  
 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVQRLAIVGAGEAGAGDILHCI 120  
 61 VLAAGEDEBDIALQIHFTLIQAFCCENDIDIVRGVQRLAIVGAGEAGAGDILHCI 120  
 121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159  
 121 LISNPEDAWKDPALFKLSLFCESRSVNDWVPSITLPE 159

US-08-652-446-12  
 Sequence 12, Application US/08652446  
 Patent No. 6057427

GENERAL INFORMATION:  
 APPLICANT: Smith, Kendall A. & Beadling, Carol  
 TITLE OF INVENTION: Nucleic Acids Encoding CR5  
 TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and  
 TITLE OF INVENTION: Expression Thereof  
 NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI  
 ADDRESS: (B) STREET: 444 South Flower St. - Suite 190  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: USA  
 ZIP: 900071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0,  
 SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/652,446  
 FILING DATE:

APPLICATION NUMBER: EP App. # 969231319.8  
 FILING DATE: 5-JUN-1998  
 APPLICATION NUMBER: PCT/US/96/09194  
 FILING DATE: 5-JUN-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/330,108  
 FILING DATE: 27-OCT-1994  
 PRIOR APPLICATION DATA: 08/463,074  
 FILING DATE: 5-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/462,337  
 FILING DATE: 5-JUN-1995  
 PRIOR APPLICATION DATA: 08/462,390  
 FILING DATE: 5-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/465,585  
 FILING DATE: 5-JUN-1995  
 PRIOR APPLICATION DATA: 08/463,081  
 APPLICATION NUMBER: 08/463,081  
 FILING DATE: 5-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/461,379  
 FILING DATE: 5-JUN-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/739,523  
 FILING DATE: 29-OCT-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Viviana Amzel, Ph. D.  
 REGISTRATION NUMBER: 30,930  
 REFERENCE/DOCKET NUMBER: FP66 40035  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 622-7700  
 TELEFAX: (213) 489-4210  
 FORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 159 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 -652-446-12

Query Match 100.0%; Score 826; DB 2; Length 159;  
 Local Similarity 100.0%; Pred. No. 6.8e-93;  
 ches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLSEVRGQDTPESTARMQAGKALHLELLLSAQRQGCCTAGVYESAKVLNVPDVTFC 60  
 1 MTLSEVRGQDTPESTARMQAGKALHLELLLSAQRQGCCTAGVYESAKVLNVPDVTFC 60  
 61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIIVAGGEAGAPGDLHCT 120  
 61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIIVAGGEAGAPGDLHCT 120  
 121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159  
 121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159

1 7  
 -534-811-7  
 uence 7, Application US/09534811  
 ent No. 661318  
 ERAL INFORMATION:  
 PLICANT: Wang, Xin Wei  
 PLICANT: Harris, Curtis C.  
 PLICANT: Fornace Jr., Albert J.  
 PLICANT: Courten, Jill D.  
 PLICANT: Zhan, Qimin  
 PLICANT: The Government of the United States of America  
 PLICANT: as represented by the Secretary of the  
 PLICANT: Department of Health and Human Services

TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45  
 TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity  
 FILE REFERENCE: 015280-3671005  
 CURRENT APPLICATION NUMBER: US/09/534,811  
 CURRENT FILING DATE: 2000-03-24  
 PRIOR APPLICATION NUMBER: 60/126,069  
 PRIOR FILING DATE: 1999-03-25  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: Patentln Ver. 2.1  
 SEQ ID NO 7  
 LENGTH: 159  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: human growth arrest and DNA-damage-inducible  
 OTHER INFORMATION: protein (hgadd45gamma).  
 US-09-534-811-7

Query Match 100.0%; Score 826; DB 2; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-93;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLSEVRGQDTPESTARMQAGKALHLELLLSAQRQGCCTAGVYESAKVLNVPDVTFC 60  
 1 MTLSEVRGQDTPESTARMQAGKALHLELLLSAQRQGCCTAGVYESAKVLNVPDVTFC 60  
 61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIIVAGGEAGAPGDLHCT 120  
 61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIIVAGGEAGAPGDLHCT 120  
 121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159  
 121 LISNPEDAMKDPALFKLSLFCESRSVNDWPSITLPE 159

RESULT 8  
 US-10-600-158-7  
 Sequence 7, Application US/10600158  
 Patent No. 7005419  
 GENERAL INFORMATION:  
 APPLICANT: Wang, Xin Wei  
 APPLICANT: Harris, Curtis C.  
 APPLICANT: Fornace Jr., Albert J.  
 APPLICANT: Courten, Jill D.  
 APPLICANT: Zhan, Qimin  
 APPLICANT: The Government of the United States of America  
 APPLICANT: as represented by the Secretary of the  
 APPLICANT: Department of Health and Human Services  
 TITLE OF INVENTION: Methods for identifying inhibitors of GADD45  
 TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity  
 FILE REFERENCE: 015280-3671005  
 CURRENT APPLICATION NUMBER: US/10/600,158  
 CURRENT FILING DATE: 2003-06-20  
 PRIOR APPLICATION NUMBER: US/09/534,811  
 PRIOR FILING DATE: 2000-03-24  
 PRIOR APPLICATION NUMBER: 60/126,069  
 PRIOR FILING DATE: 1999-03-25  
 NUMBER OF SEQ ID NOS: 32  
 SOFTWARE: Patentln Ver. 2.1  
 SEQ ID NO 7  
 LENGTH: 159  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: human growth arrest and DNA-damage-inducible  
 OTHER INFORMATION: protein (hgadd45gamma)  
 US-10-600-158-7

Query Match 100.0%; Score 826; DB 3; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 6.8e-93;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MTLSEVRGQDTPESTARMQAGKALHLELLLSAQRQGCCTAGVYESAKVLNVPDVTFC 60

1 MTLPEVRGQTVPESTRMGAGKALHELLSQRQCLNRYGYESAKVLNVDPDNTFC 60  
61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDYRVGVQRLAAIVAGEBEGAPGDHCT 120  
61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDYRVGVQRLAAIVAGEBEGAPGDHCT 120  
121 LISPNEDAMKDPALKEKLSLFCESRSRVNVPISITLPE 159  
121 LISPNEDAMKDPALKEKLSLFCESRSRVNVPISITLPE 159

IT 9  
-949-016-9744  
nuence 9744, Application US/09949016

GENERAL INFORMATION:

PPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 LE REFERENCE: CL001307

LE REFERENCE: CL001307

IRRENT APPLICATION NUMBER: US/09/949,016

IRRENT FILING DATE: 2000-04-14

APPLICATOR: 60/241,755

FOR FILING DATE: 2000-10-20  
FOR ADDITION NUMBER: 60/

FOR APPLICATION NUMBER: 60/237,168  
FILING DATE: 2000-10-03

FOR FILING DATE: 2000-10-03  
APPLICATION NUMBER: 60/231,498

FOR FILING DATE: 2000-09-08

NUMBER OF SEO ID NOS: 20701

```

)FTWARE: FastSEQ for Windows Version 4.0

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2 ID NO 9744

i,LENGTH: 165

TYPE: PRT

ORGANISM: Human

( )-949-016-9744

Very Match	100.0%;	Score 826;	DB 2;	Length 165;
------------	---------	------------	-------	-------------

1 MTLLEVRKQDVTPESTIARMQAGAKALHELLLSAQROGCLTAGYIEAKIYLANDPNNVTF 60  
7 MTLLEVRKQDVTPESTIARMQAGAKALHELLLSAQROGCLTAGYIEAKIYLANDPNNVTF 66  
61 VLAAGEDEBEGIALQIHFTLIQAFCNCNDIDIVRVGDVRLAIVAGEEAGAPGLHCI 120  
67 VLAAGEDEBEGIALQIHFTLIQAFCNCNDIDIVRVGDVRLAIVAGEEAGAPGLHCI 126  
121 LISNPNEADKQPALKEKLSLPCESRSRVNVMVSIPLPE 159  
127 LISNPNEADKQPALKEKLSLPCESRSRVNVMVSIPLPE 165

IT 10  
4-797-831A-1  
Influence 1, Application US/08797831A  
ent No. 5808031

GENERAL INFORMATION:

APPLICANT: Mikio, SUZUKI

APPLICANT: Takeshi, WATANABE

APPLICANT: Tsutomu, FUJIWARA  
TITLE OF INVENTION: CDD17 GENE

NUMBER OF SENTENCES: 3

NUMBER OF SEQUENCES: 2

ADDRESSEE: Suphrue,

STREET: 2100 Pennsylvania Avenue, N.W.

CITY: Washington

COUNTRY: United States

ZIP: 20037-3202

COMPUTER READABLE

MEDIUM TYPE: Floppy

COMPUTER: IBM PC compatible

```

? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent In Release #1.24
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/797,831A
? FILING DATE:
? CLASSIFICATION: 536
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (202) 293-7060
? TELEFAX: (202) 253-7860
? TELERX: 6491103
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 159 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
?
US-08-797-831A-1

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Query Match	98.5%	Score 814	DB 1	length 159
Best Local Similarity	98.7%	Pred. No.	2e-91	
Matches 157	Conservative	0	Mismatches	2
			Indels	0
			Gaps	0

QY 1 MTLBEVRQDPIVPESTAMQAGAKLHLLLSAQSOGCTACGYESAKLVNDPQNVATFC 60

Db 1 MTLBEVRQDPIVPESTAMQAGAKLHLLLSAHQGGCTACGYESAKLVNDPQNVATFC 60

QY 61 VLAAGEEDGDIALOIHFTLLIOAFCCENDIDIVRVGDVORLAIYVAGEEAGAPGDLHCI 120

Db 61 VLAAGEEDGDIALOIHFTLLIOAFCCENDIDIVRVGDVORLAIYVAGEEAGAPGDLHCI 120

QY 121 LISNPEDAMKQPALEKLSLFCESRSRVNDWVPSTLPE 159

Db 121 LISNPEDAMKQPALEKLSLFCESRSRVNDWVPSTLPE 159

```

      RESULT 11
US-09-879-833-2
; Sequence 2, Application US/09879833
; Patent No. 6573371
; GENERAL INFORMATION:
; APPLICANT: PARK, Chong-Hun; SAMYANG GENEX CORPORATION
; TITLE OF INVENTION: CANCER DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL D
; TITLE OF INVENTION: FERTILIZATION SPECIFIC SYG972 GENE AND GENOMIC DNA AND PROMOTER
; TITLE OF INVENTION: EREOP
; FILE REFERENCE: PA/SYG/99601
; CURRENT APPLICATION NUMBER: US/09/879,833
; CURRENT FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: KOR-54933
; PRIOR FILING DATE: 1998-12-12
; PRIOR APPLICATION NUMBER: KR 63958
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: KOBATIN 1.5
; SEQ ID NO 2
; LENGTH: 160
; TYPE: prt
; ORGANISM: HL60 cell line
US-09-879-833-2
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Query Match	98.2%	Score 811;	DB 2;	length 160;
Best Local Similarity	98.7%	Pred. No.	4,7e-91;	
Matches 15/;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

Qy 1 MTLVEVRGDDVTPESTARNOGAGKALHLLLSAQOGCTTAVGVSASAKLVNDPDNVTC 60

Db 1 MTLVEVRGDDVTPESTARNOGAGKALHLLLSAQOGCTTAVGVSASAKLVNDPDNVRC 60

Qy 61 VLAAGEBEDGDIALQIHFTLLIQAFCCENDIDIVRVGDVQRLAIVAGEEAGAPGDHCT 120

Db 61 VLAAGEVGVGDIALQIHFTLLIQAFCCENDIDIVRVGDVQRLAIVAGEEAGAPGDHCT 120

Qy 121 LISNPEDAKDPALHEKLSLFCSEERSVNDWVPSTLPE 159

121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159

T 12

-602-208-3  
ence 3, Application US/08602208  
ent No. 5866332

GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin Graeme

APPLICANT: Au-Young, Janice

APPLICANT: Sellhamer, Jeffrey J.

TITLE OF INVENTION: NOVEL HUMAN MYELOID TERMINAL

TITLE OF INVENTION: DIFFERENTIATION RESPONSE GENE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94303

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/602,208

FILING DATE: Filed Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/221,531

FILING DATE: 02-FEB-1994

ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.

REGISTRATION NUMBER: 33,954

REFERENCE/DOCKET NUMBER: PF-0054 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-852-0195

TELEX:

FORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 165 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: Myeloid Terminal

-602-208-3

ty Match 55.4%; Score 457.5; DB 1; Length 165;

t Local Similarity 54.5%; Pred. No. 9.6e-48;

ches 91; Conservative 22; Mismatches 43; Indels 11; Gaps 2;

1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

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1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

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1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

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1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60

GENERAL INFORMATION:

APPLICANT: Wang, Xin Wei

APPLICANT: Harris, Curtis C.

APPLICANT: Fornace Jr., Albert J.

APPLICANT: Courten, Jill D.

APPLICANT: Zhan, Qimin

APPLICANT: The Government of the United States of America

as represented by the Secretary of the

Department of Health and Human Services

TITLE OF INVENTION: Methods for identifying inhibitors of GADD45

TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity

FILE REFERENCE: 015280-367100US

CURRENT APPLICATION NUMBER: US/09/534,811

CURRENT FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: US 60/126,069

PRIOR FILING DATE: 1999-03-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 165

TYPE: PRT

ORGANISM: Homo sapiens

US-09-534-811-2

Query Match

Best Local Similarity 54.5%;

Pred. No. 9.6e-48;

Matches 91; Conservative 22;

Mismatches 43; Indels 11; Gaps 2;

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1 MTLSEVRGQDTPESTARMOGAKALHLLLSAORQGLTAGYESAKVLPDNTVFC 60



ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0054 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0195  
TELEFAX: 415-852-0195  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 165 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: Myeloid Terminal  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
1-208-206-3

Any Match 55.4%; Score 457.5; DB 2; Length 165;  
Local Similarity 54.5%; Pred. No. 9,6e-48;  
Conservative 22; Mismatches 43; Indels 11; Gaps 2;

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58 LLAADDDDDVALQIHFTLLIQAFCCENDINILRVSNPRLAELLLETTDAGPAAEGAB 117  
113 APGDLCILISNPEDAKMDPALEKLSLFCESRSRVNDVPSITLPE 159  
118 QPPDLHCVLVTPHSSQWKDPALSLICFCRESRYMDQWVPVINTPE 164

15  
1-600-158-2  
Invention 2, Application US/10600158  
Inventor No. 7005419  
Inventor INFORMATION:  
APPLICANT: Wang, Xin Wei  
APPLICANT: Harris, Curtis C.  
APPLICANT: Fornace Jr., Albert J.  
APPLICANT: Courten, Jill D.  
APPLICANT: Zhan, Qimin  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by the Secretary of the  
DEPARTMENT OF HEALTH AND HUMAN SERVICES  
TITLE OF INVENTION: Methods for identifying inhibitors of GADD45  
TITLE OF INVENTION: Polypeptide activity, and inhibitors of such activity  
FILE REFERENCE: 015280-367100US  
CURRENT APPLICATION NUMBER: US/10/600,158  
PRIOR FILING DATE: 2003-06-20  
PRIOR APPLICATION NUMBER: US/09/534,811  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: US 60/126,069  
PRIOR FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
ID NO 2  
LENGTH: 165  
TYPE: PRT  
ORGANISM: Homo sapiens  
1-600-158-2

Any Match 55.4%; Score 457.5; DB 3; Length 165;  
Local Similarity 54.5%; Pred. No. 9,6e-48;  
Conservative 22; Mismatches 43; Indels 11; Gaps 2;

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Qy 61 VLAAGEDEGDIALQIHFTLLIQAFCCENDIDIVRGDVORLAIV-----GAGEAG 112  
Db 58 LLAADDDDDVALQIHFTLLIQAFCCENDINILRVSNPRLAELLLETTDAGPAAEGAB 117  
Qy 113 APGDLCILISNPEDAKMDPALEKLSLFCESRSRVNDVPSITLPE 159  
Db 118 QPPDLHCVLVTPHSSQWKDPALSLICFCRESRYMDQWVPVINTPE 164

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Job time: 27 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

Protein - protein search, using sw model

June 2, 2006, 22:37:54 ; Search time 178 Seconds  
(Without alignments)  
413.771 Million cell updates/sec

US-10-089-641-2  
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2097797 seqs, 463214858 residues

number of hits satisfying chosen parameters: 2097797

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processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Published Applications AA Main:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_PUBCOMB.pep.\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_PUBCOMB.pep.\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_PUBCOMB.pep.\*
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- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Score	Query Match	length	DB	ID	Description
826	100.0	159	4	US-10-263-330-10	Sequence 10, Appl
826	100.0	159	4	US-10-626-905-10	Sequence 10, Appl
826	100.0	159	5	US-10-287-436A-441	Sequence 441, Appl
826	100.0	159	5	US-10-287-436A-1142	Sequence 1142, Appl
826	100.0	159	5	US-10-631-467-560	Sequence 560, Appl
826	100.0	160	5	US-10-821-234-1127	Sequence 1127, Appl
811	98.2	160	3	US-09-879-833-2	Sequence 2, Appl
787	95.3	159	4	US-10-263-330-12	Sequence 12, Appl
787	95.3	159	4	US-10-626-905-12	Sequence 12, Appl
787	95.3	159	5	US-10-631-467-1387	Sequence 1387, Appl
737	89.2	141	4	US-10-087-192-1356	Sequence 1356, Appl
710	86.0	158	4	US-10-087-192-1353	Sequence 1353, Appl
541	65.5	110	5	US-10-617-316-176	Sequence 176, Appl
457.5	55.4	165	4	US-10-263-330-6	Sequence 6, Appl
457.5	55.4	165	4	US-10-626-905-6	Sequence 6, Appl
451.5	54.7	165	4	US-10-263-330-4	Sequence 4, Appl
451.5	54.7	165	4	US-10-263-330-8	Sequence 8, Appl
451.5	54.7	165	4	US-10-626-905-8	Sequence 8, Appl
447	54.1	160	5	US-10-821-234-1305	Sequence 1305, Appl
436	52.8	160	4	US-10-626-905-4	Sequence 4, Appl
420.5	50.9	161	4	US-10-263-330-2	Sequence 2, Appl
420.5	50.9	161	4	US-10-626-905-2	Sequence 2, Appl
391	47.3	193	3	US-09-925-298-713	Sequence 713, Appl
391	47.3	193	3	US-10-102-806-713	Sequence 713, Appl
226	27.4	72	6	US-11-032-794-36	Sequence 36, Appl
226	27.4	72	6	US-11-000-365-36	Sequence 36, Appl
157	19.0	163	6	US-11-097-143-4575	Sequence 4575, Appl

28	116	14.0	27	6	US-11-032-794-2	Sequence 2, Appli
29	116	14.0	27	6	US-11-000-365-2	Sequence 2, Appli
30	115.5	13.5	109	3	US-09-805-020-42	Sequence 42, Appl
31	111.5	13.5	49	4	US-10-425-115-282840	Sequence 282840, Appl
32	107	13.0	41	4	US-10-263-828-133	Sequence 133, App
33	103.5	12.5	132	5	US-10-821-234-1676	Sequence 1676, App
34	102	12.3	20	6	US-11-032-794-39	Sequence 39, Appl
35	102	12.3	20	6	US-11-000-365-39	Sequence 39, Appl
36	98	11.9	20	6	US-11-032-794-42	Sequence 42, Appl
37	98	11.9	20	6	US-11-000-365-42	Sequence 42, Appl
38	96	11.6	396	4	US-10-156-761-7971	Sequence 7971, App
39	94	11.4	349	4	US-10-282-122A-51953	Sequence 51953, A
40	92	11.1	18	6	US-11-032-794-3	Sequence 3, Appli
41	92	11.1	18	6	US-11-000-365-3	Sequence 3, Appli
42	91	11.0	354	4	US-10-282-122A-53057	Sequence 53057, A
43	90	10.9	183	5	US-10-450-763-34923	Sequence 34923, A
44	87	10.5	91	4	US-10-363-829-272	Sequence 272, App
45	86.5	10.5	132	4	US-10-116-275-256	Sequence 256, App

## ALIGNMENTS

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RESULT 1
US-10-263-330-10
; Sequence 10, Application US/10263330
; Publication No. US20030077262A1
; GENERAL INFORMATION:
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: ZAZZERONI, FRANCESCA
; APPLICANT: PAPA, SALVATORE
; TITLE OF INVENTION: MODULATORS OF APOPTOSIS
; FILE REFERENCE: ARCD:379USP1
; CURRENT APPLICATION NUMBER: US/10/263,330
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/60/326,492
; PRIOR FILING DATE: 2001-10-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-263-330-10

Query Match      100.0%; Score 826; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 3e-87;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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   |||||

QY 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159
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US-10-626-905-10
; Sequence 10, Application US/10626905
; Publication No. US20040121463A1
; GENERAL INFORMATION:
; APPLICANT: FRANZOSO, GUIDO
; APPLICANT: DESMAELE, ENRICO
; APPLICANT: ZAZZERONI, FRANCESCA
; APPLICANT: PAPA, SALVATORE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS

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LE REFERENCE: 21459-94575  
 RECENT APPLICATION NUMBER: US/10/626,905  
 RECENT FILING DATE: 2003-07-25  
 RECENT APPLICATION NUMBER: PCT/US02/31548  
 FOR FILING DATE: 2002-10-02  
 FOR FILING DATE: 2002-10-02  
 FOR FILING DATE: 2002-10-02  
 FOR FILING DATE: 2002-10-02  
 FOR FILING DATE: 2001-10-12  
 FOR FILING DATE: 2001-10-12  
 FOR FILING DATE: 2001-10-12  
 FOR FILING DATE: 2001-10-02  
 MEMBER OF SEQ ID NOS: 53  
 FTWAVE: PatentIn ver. 3.2  
 ID NO 10  
 LENGTH: 159  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 -626-905-10

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 Local Similarity 100.0%; Pred. No. 3e-87;  
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 Application US/10287436A  
 Publication No. US20050202421A1  
 SERIAL INFORMATION:  
 APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER  
 TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF  
 TITLE OF INVENTION: RHEUMATOID ARTHRITIS  
 LE REFERENCE: 10872.514696  
 RECENT FILING DATE: 2002-10-31  
 RECENT APPLICATION NUMBER: US/10/287,436A  
 FOR FILING DATE: 2001-10-31  
 FOR FILING DATE: 2001-10-31  
 MEMBER OF SEQ ID NOS: 146  
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 ID NO 441  
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RESULT 4  
 US-10-287-436A-1142  
 Sequence 1142, Application US/10287436A  
 Publication No. US20050202421A1  
 GENERAL INFORMATION:  
 APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER  
 TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF  
 TITLE OF INVENTION: RHEUMATOID ARTHRITIS  
 FILE REFERENCE: 10872.514696  
 CURRENT APPLICATION NUMBER: US/10/287,436A  
 CURRENT FILING DATE: 2002-10-31  
 PRIOR FILING DATE: 2001-10-31  
 PRIOR FILING DATE: 2001-10-31  
 NUMBER OF SEQ ID NOS: 146  
 SOFTWARE: PatentIn ver. 3.2  
 SEQ ID NO 1142  
 LENGTH: 159  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-287-436A-1142

Query Match 100.0%; Score 826; DB 5; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 3e-87;  
 Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
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 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
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 Db 121 LISNPEDAMKDPALFKLSLFCESRSVNDWVPSITLPE 159  
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RESULT 5  
 US-10-631-467-560  
 Sequence 560, Application US/10631467  
 Publication No. US20050208496A1  
 GENERAL INFORMATION:  
 APPLICANT: Genox Research Inc.  
 TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive  
 TITLE OF INVENTION: disease  
 FILE REFERENCE: 3462.1005-000  
 CURRENT APPLICATION NUMBER: US/10/631,467  
 CURRENT FILING DATE: 2003-07-31  
 PRIOR FILING DATE: 2003-07-212  
 PRIOR FILING DATE: 2003-03-20  
 PRIOR APPLICATION NUMBER: JP 2002-229312  
 PRIOR FILING DATE: 2002-08-06  
 NUMBER OF SEQ ID NOS: 2086  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 560  
 LENGTH: 159  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-631-467-560

Query Match 100.0%; Score 826; DB 5; Length 159;  
 Best Local Similarity 100.0%; Pred. No. 3e-87;  
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0-821-234-1127
quence 1127, Application US/10821234
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GENERAL INFORMATION:
PLICANT: Labat, Ivan
PLICANT: Stache-Crain, Birgit
PLICANT: Andammani, Susan
PLICANT: Tang, X. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
PRIORITY FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIORITY FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pc_seq_genes Version 1.0
) ID NO 1127
LENGTH: 165
TYPE: PRF
ORGANISM: Homo sapiens
0-821-234-1127

HIT 7
9-879-833-2
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tent No. US20020055107A1
GENERAL INFORMATION:
PLICANT: Park, Chong-Hun; SAMYANG GENEX CORPORATION
TITLE OF INVENTION: CANCER DIAGNOSIS METHOD USING CELL GROWTH INHIBITING AND CELL DIFFERENTIATION INDUCING AGENTS
TITLE OF INVENTION: PERCENTIATION SPECIFIC SYG972 GENE AND GENOMIC DNA AND PROMOTER TACTILE OF INVENTION: ERROR
FILE REFERENCE: PA/SYG/99601
CURRENT APPLICATION NUMBER: US/09/879,833
PRIORITY FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: KR 54933
PRIORITY FILING DATE: 1998-12-12
PRIOR APPLICATION NUMBER: KR 63958
PRIORITY FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 3
SOFTWARE: KOPATIN 1.5
) ID NO 2
LENGTH: 160
TYPE: PRF
ORGANISM: HL60 cell line
9-879-833-2

HIT Match          98.2%; Score 811; DB 3; Length 160;
nt Local Similarity 98.7%; Pred. No. 1,7e+85;
ches 157; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db	1	MTLEEVVGQDTPVESTARMQAGKALHLLLSAORQCLTAGYVESAKVLNVPDNTVFC	60
QY	61	VLAAGEEDDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAIVGAGEBAGAPGDHICI	120
Db	61	VLAAGEEVEDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAIVGAGEBAGAPGDHICI	120
QY	121	LISPNEDAMKDPALFKLSLFCESRSRVNDWVBSITLPE	159
Db	121	LISPNEDAMKDPALFKLSLFCESRSRVNDWVBSITLPE	159
RESULT 8			
US-10-263-330-12			
; Sequence 12, Application US/10263330			
; Publication No. US20030077262A1			
GENERAL INFORMATION:			
APPLICANT: FRANZOSO, GUIDO			
APPLICANT: DESMAELE, ENRICO			
APPLICANT: ZAZZERONI, FRANCESCA			
APPLICANT: PAPA, SALVATORE			
TITLE OF INVENTION: MODULATORS OF APOPTOSIS			
FILE REFERENCE: ARCD:379USP1			
CURRENT APPLICATION NUMBER: US/10/263,330			
CURRENT FILING DATE: 2002-10-02			
PRIOR APPLICATION NUMBER: US/60/326,492			
PRIOR FILING DATE: 2001-10-02			
NUMBER OF SEQ ID NOS: 15			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 12			
LENGTH: 159			
TYPE: PRT			
ORGANISM: Mus musculus			
US-10-263-330-12			
Query Match			
Best Local Similarity 95.3%; Score 787; DB 4; Length 159;			
Matches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;			
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Db	1	MTLEEVVGQDTPVESTARMQAGKALHLLLSAORQCLTAGYVESAKVLNVPDNTVFC	60
QY	61	VLAAGEEDDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAIVGAGEBAGAPGDHICI	120
Db	61	VLAAGEEVEDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAIVGAGEBAGAPGDHICI	120
QY	121	LISPNEDAMKDPALFKLSLFCESRSRVNDWVBSITLPE	159
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RESULT 9			
US-10-626-905-12			
; Sequence 12, Application US/10626905			
; Publication No. US20040121463A1			
GENERAL INFORMATION:			
APPLICANT: FRANZOSO, GUIDO			
APPLICANT: DESMAELE, ENRICO			
APPLICANT: ZAZZERONI, FRANCESCA			
APPLICANT: PAPA, SALVATORE			
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING APOPTOSIS			
FILE REFERENCE: 21459-94575			
CURRENT APPLICATION NUMBER: US/10/626,905			
CURRENT FILING DATE: 2003-07-25			
PRIOR APPLICATION NUMBER: PCT/US02/31548			
PRIOR FILING DATE: 2002-10-02			
PRIOR APPLICATION NUMBER: 10/263,330			
PRIOR FILING DATE: 2002-10-02			
PRIOR APPLICATION NUMBER: 60/328,811			
PRIOR FILING DATE: 2001-10-12			

FOR APPLICATION NUMBER: 60/326,492  
 FOR FILING DATE: 2001-10-02  
 NUMBER OF SEQ ID NOS: 53  
 FTWAB: Patent Ver. 3.2  
 ID NO: 12  
 LENGTH: 159  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 -626-905-12

cy Match 95.3%; Score 787; DB 4; Length 159;  
 Local Similarity 95.6%; Pred. No. 1e-82;  
 ches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 MTLLEVRGQDTPESTARMOGAGKALHELLLSAQRQCLTAGYVESAKVLNVDPDNVTFC 60  
 1 MTLLEVRGQDTPESTARMOGAGKALHELLLSAQRQCLTAGYVESAKVLNVDPDNVTFC 60  
 61 VLAAGEDEBDDIALQIHFTLQAFCCENDIDIVRGDVORLAIVGAGEBAGAPGDLHCT 120  
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 121 LISNPEDTWKDPALFKLSLFCESRSFNDWVPSITLPE 159  
 121 LISNPEDTWKDPALFKLSLFCESRSFNDWVPSITLPE 159

r 10  
 -631-467-1387  
 Application US/10631467  
 Publication No. US20050208496A1  
 SERIAL INFORMATION:  
 APPLICANT: Genox Research Inc.  
 TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p  
 TLE OF INVENTION: disease  
 LE REFERENCE: 3462, 1005-000  
 PRESENT APPLICATION NUMBER: US/10/631,467  
 PRESENT FILING DATE: 2003-07-31  
 FOR APPLICATION NUMBER: JP 2003-077212  
 FOR FILING DATE: 2003-03-20  
 FOR APPLICATION NUMBER: JP 2002-229312  
 FOR FILING DATE: 2002-08-06  
 NUMBER OF SEQ ID NOS: 2086  
 FTWAB: Patent Ver. 3.1  
 ID NO: 1387  
 LENGTH: 159  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 -631-467-1387

cy Match 95.3%; Score 787; DB 5; Length 159;  
 Local Similarity 95.6%; Pred. No. 1e-82;  
 ches 152; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 MTLLEVRGQDTPESTARMOGAGKALHELLLSAQRQCLTAGYVESAKVLNVDPDNVTFC 60  
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 61 VLAAGEDEBDDIALQIHFTLQAFCCENDIDIVRGDVORLAIVGAGEBAGAPGDLHCT 120  
 61 VLAAGEDEBDDIALQIHFTLQAFCCENDIDIVRGDVORLAIVGAGEBAGAPGDLHCT 120  
 61 VLAAGEDEBDDIALQIHFTLQAFCCENDIDIVRGDVORLAIVGAGEBAGAPGDLHCT 120  
 121 LISNPEDTWKDPALFKLSLFCESRSFNDWVPSITLPE 159  
 121 LISNPEDTWKDPALFKLSLFCESRSFNDWVPSITLPE 159

r 11  
 -087-192-1356  
 Application US/10087192  
 Publication No. US20020182586A1  
 SERIAL INFORMATION:  
 APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.  
 TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
 TITLE OF INVENTION: CANCER  
 FILE REFERENCE: 529452000122  
 CURRENT APPLICATION NUMBER: US/10/087,192  
 PRIOR FILING DATE: 2002-03-01  
 PRIOR APPLICATION NUMBER: US 09/747,377  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: US 09/798,586  
 PRIOR FILING DATE: 2001-03-02  
 NUMBER OF SEQ ID NOS: 2059  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 1356  
 LENGTH: 141  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-087-192-1356

Query Match 89.2%; Score 737; DB 4; Length 141;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-77;  
 Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 MOGAGKALHELLLSAQRQCLTAGYVESAKVLNVDPDNVTFCVLAAGEDEBDDIALQIHFT 78  
 1 MOGAGKALHELLLSAQRQCLTAGYVESAKVLNVDPDNVTFCVLAAGEDEBDDIALQIHFT 78  
 61 TLIQAFCCENDIDIVRGDVORLAIVGAGEBAGAPGDLHCTLISNPEDTWKDPALFKL 120  
 61 TLIQAFCCENDIDIVRGDVORLAIVGAGEBAGAPGDLHCTLISNPEDTWKDPALFKL 120  
 139 SLFCESRSFNDWVPSITLPE 159  
 121 SLFCESRSFNDWVPSITLPE 141

RESULT 12  
 US-10-087-192-1353  
 Sequence 1353, Application US/10087192  
 Publication No. US20020182586A1  
 GENERAL INFORMATION:  
 APPLICANT: Morris, David W.  
 APPLICANT: Engelhard, Eric K.  
 TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
 TITLE OF INVENTION: CANCER  
 FILE REFERENCE: 529452000122  
 PRESENT APPLICATION NUMBER: US/10/087,192  
 PRESENT FILING DATE: 2002-03-01  
 PRIOR APPLICATION NUMBER: US 09/747,377  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: US 09/798,586  
 PRIOR FILING DATE: 2001-03-02  
 NUMBER OF SEQ ID NOS: 2059  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO: 1353  
 LENGTH: 158  
 TYPE: PRT  
 ORGANISM: Mus musculus  
 US-10-087-192-1353

Query Match 96.0%; Score 710; DB 4; Length 158;  
 Best Local Similarity 96.5%; Pred. No. 8.7e-74;  
 Matches 136; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

19 MOGAGKALHELLLSAQRQCLTAGYVESAKVLNVDPDNVTFCVLAAGEDEBDDIALQIHFT 78  
 18 MOGAGKALHELLLSAQRQCLTAGYVESAKVLNVDPDNVTFCVLAAGEDEBDDIALQIHFT 77  
 79 TLIQAFCCENDIDIVRGDVORLAIVGAGEBAGAPGDLHCTLISNPEDTWKDPALFKL 138  
 78 TLIQAFCCENDIDIVRGDVORLAIVGAGEBAGAPGDLHCTLISNPEDTWKDPALFKL 137  
 139 SLFCESRSFNDWVPSITLPE 159



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Protein - protein search, using sw model

June 2, 2006, 22:37:57 ; Search time 9 seconds  
(without alignments)  
204.318 Million cell updates/sec

US-10-089-641-2  
1 MTLSEVRGQDVTPESTARMQ.....LFCESRSVNDWPSITLPE 159

Gapop 10.0 , Gapext 0.5

58871 seqs, 11565156 residues

number of hits satisfying chosen parameters: 58871

DB seq length: 0  
DB seq length: 200000000

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Published Applications\_AA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US09\_NEW\_PUB pep:\*
- 2: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US06\_NEW\_PUB pep:\*
- 3: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US07\_NEW\_PUB pep:\*
- 4: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US08\_NEW\_PUB pep:\*
- 5: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US10\_NEW\_PUB pep:\*
- 6: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_NEW\_PUB pep:\*
- 7: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US11\_NEW\_PUB pep:\*
- 8: /EMC\_Celerra\_SIDS3/prodata/2/pubppaa/US06\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Score	Query Match	Length	ID	Description
826	100.0	159	US-11-297-160-7	Sequence 7, Appl
457.5	55.4	165	US-10-505-928-797	Sequence 797, Appl
457.5	55.4	165	US-11-297-160-2	Sequence 2, Appl
451.5	54.7	165	US-11-297-160-8	Sequence 8, Appl
447.5	54.1	160	US-11-297-160-6	Sequence 6, Appl
436.5	52.8	165	US-11-297-160-9	Sequence 9, Appl
200	24.2	46	US-11-297-160-16	Sequence 16, Appl
184	22.3	41	US-11-297-160-32	Sequence 32, Appl
164	19.9	38	US-11-297-160-17	Sequence 17, Appl
157	19.0	36	US-11-297-160-31	Sequence 31, Appl
143	17.3	34	US-11-297-160-10	Sequence 10, Appl
126	15.3	34	US-11-297-160-11	Sequence 11, Appl
123	14.9	27	US-11-297-160-23	Sequence 23, Appl
120	14.5	26	US-11-297-160-22	Sequence 22, Appl
104	12.6	34	US-11-297-160-12	Sequence 12, Appl
98	11.9	26	US-11-297-160-18	Sequence 18, Appl
95	11.5	34	US-11-297-160-13	Sequence 13, Appl
94	11.4	26	US-11-297-160-21	Sequence 21, Appl
94	11.4	352	US-10-953-349-9817	Sequence 9817, Ap
94	11.4	376	US-10-953-349-9816	Sequence 9816, Ap
94	11.4	430	US-10-953-349-9815	Sequence 9815, Ap
83	10.0	21	US-11-297-160-19	Sequence 19, Appl
75	9.1	1099	US-10-506-630A-41	Sequence 41, Appl
72	8.7	21	US-11-297-160-20	Sequence 20, Appl
71.5	8.7	482	US-10-953-349-26529	Sequence 26529, A

26	71.5	8.7	576	6	US-10-953-349-26528	Sequence 26528, A
27	71.5	8.7	617	6	US-10-953-349-26527	Sequence 26527, A
28	71.5	8.6	212	6	US-10-953-349-3470	Sequence 3470, Ap
29	67.5	8.2	239	6	US-10-953-349-5219	Sequence 5219, Ap
30	66.5	8.1	109	6	US-10-953-349-3623	Sequence 3623, Ap
31	66	8.0	289	6	US-10-953-349-30066	Sequence 30066, A
32	66	8.0	299	6	US-10-953-349-30065	Sequence 30065, A
33	66	8.0	367	6	US-10-953-349-21630	Sequence 21630, A
34	66	8.0	377	6	US-10-953-349-30064	Sequence 30064, A
35	66	8.0	383	6	US-10-953-349-21629	Sequence 21629, A
36	65.5	7.9	334	6	US-10-953-349-2021	Sequence 2021, Ap
37	65.5	7.9	443	6	US-10-953-349-2020	Sequence 2020, Ap
38	65.5	7.9	453	6	US-10-953-349-2019	Sequence 2019, Ap
39	65	7.9	17	7	US-11-297-160-24	Sequence 24, Appl
40	64.5	7.8	154	6	US-10-953-349-13851	Sequence 13851, A
41	64.5	7.8	155	6	US-10-953-349-13850	Sequence 13850, A
42	64.5	7.8	160	6	US-10-953-349-13849	Sequence 13849, A
43	63.5	7.7	1289	7	US-11-293-697-2971	Sequence 2971, Ap
44	62.5	7.6	223	6	US-10-953-349-20462	Sequence 20462, A
45	62.5	7.6	231	6	US-10-953-349-20461	Sequence 20461, A

# ALIGNMENTS

RESULT 1  
US-11-297-160-7  
Sequence 7, Application US/11297160  
Publication No. US2006008888A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Xin Wei  
APPLICANT: Harris, Curtis C.  
APPLICANT: Fornace Jr., Albert J.  
APPLICANT: Courseen, Jill D.  
APPLICANT: Zhan, Qimin  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by the Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity  
FILE REFERENCE: 015280-367100US  
CURRENT APPLICATION NUMBER: US/11/297,160  
CURRENT FILING DATE: 2005-12-07  
PRIOR APPLICATION NUMBER: US/10/600,158  
PRIOR FILING DATE: 2003-06-20  
PRIOR APPLICATION NUMBER: US/09/534,811  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: US 60/126,069  
PRIOR FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 159  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: human growth arrest and DNA-damage-inducible  
US-11-297-160-7  
Query Match 100.0%; Score 826; DB 7; Length 159;  
Best Local Similarity 100.0%; Pred. No. 5.5e-82;  
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTLSEVRGQDVTPESTARMQAGKALHELLISAQROGCTAGVYESAKVNVDPNTFC 60  
DB 1 MTLSEVRGQDVTPESTARMQAGKALHELLISAQROGCTAGVYESAKVNVDPNTFC 60  
QY 61 VLAAGEDESDIALQIHFTLLIOAFCCENDIDYRVGVORLAIVGAGEGAGDILHCT 120  
DB 61 VLAAGEDESDIALQIHFTLLIOAFCCENDIDYRVGVORLAIVGAGEGAGDILHCT 120  
QY 121 LISNPEDAKMPALEKLSLFCESRSVNDWPSITLPE 159

121 L1SNPNEDAMKDPALFKLSLFCESRSVNDWVPSTLPE 159

1 2  
-505-928-797  
Sequence 797, Application US/10505928  
Publication No. US20060088532A1  
GENERAL INFORMATION:  
APPLICANT: Ludwig Institute for Cancer Research et al.  
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
LE REFERENCE: 28967/39178  
CURRENT APPLICATION NUMBER: US/10/505,928  
PARENT FILING DATE: 2004-08-27  
FOR FILING DATE: 2002-03-07  
MEMBER OF SEQ ID NOS: 866  
SOFTWARE: PatentIn 3.2  
ID NO 797  
LENGTH: 165  
TYPE: PRT  
ORGANISM: Homo sapiens  
-505-928-797

Local Match 55.4%; Score 457.5; DB 6; Length 165;  
Local Similarity 54.5%; Pred. No. 2.5e-42; Indels 11; Gaps 2;  
Conservative 22; Mismatches 43; Indels 11; Gaps 2;  
1 MTLSEVRGQDTPVPESTARMOGAKALHELLLSAOROGCLTAGYSAKVLNPDVPTFC 60  
1 MTLSEFSAGE---QKTERMDKVGDALAEVLSKALSQRITVGVYEAKLINDPNDVVLJC 57  
61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIV-----GAGEBAG 112  
58 LLAADDDDDRDVALQIHFTLIQAFCCENDINILRVSNPRLAELLLETDAGPAASEGAE 117  
113 APGDLCILISNPNEDAMKDPALFKLSLFCESRSVNDWVPSTLPE 159  
118 QPDLHCVLVTPHSSQWKDPALSLICFCRESRYMDQWVPVNIPE 164

1 3  
-297-160-2  
Sequence 2, Application US/11297160  
Publication No. US20060088888A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Xin Wei  
APPLICANT: Harris, Curtis C.  
APPLICANT: Fornace Jr., Albert J.  
APPLICANT: Courten, Jill D.  
APPLICANT: Zhan, Qimin  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by the Secretary of the  
TITLE OF INVENTION: Department of Health and Human Services  
TITLE OF INVENTION: Methods for identifying inhibitors of GADD45  
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity  
LE REFERENCE: 015280-367100US  
CURRENT APPLICATION NUMBER: US/11/297,160  
PARENT FILING DATE: 2005-12-07  
FOR FILING DATE: 2003-06-20  
FOR APPLICATION NUMBER: US/09/534,811  
FOR FILING DATE: 2000-03-24  
FOR APPLICATION NUMBER: US 60/126,069  
FOR FILING DATE: 1999-03-25  
MEMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
ID NO 2  
LENGTH: 165  
TYPE: PRT  
ORGANISM: Homo sapiens  
-297-160-2

Query Match 55.4%; Score 457.5; DB 7; Length 165;  
Best Local Similarity 54.5%; Pred. No. 2.5e-42;  
Matches 91; Conservative 22; Mismatches 43; Indels 11; Gaps 2;

QY 1 MTLSEVRGQDTPVPESTARMOGAKALHELLLSAOROGCLTAGYSAKVLNPDVPTFC 60  
1 MTLSEFSAGE---QKTERMDKVGDALAEVLSKALSQRITVGVYEAKLINDPNDVVLJC 57  
Db 61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIV-----GAGEBAG 112  
58 LLAADDDDDRDVALQIHFTLIQAFCCENDINILRVSNPRLAELLLETDAGPAASEGAE 117  
QY 113 APGDLCILISNPNEDAMKDPALFKLSLFCESRSVNDWVPSTLPE 159  
118 QPDLHCVLVTPHSSQWKDPALSLICFCRESRYMDQWVPVNIPE 164  
Db

RESULT 4

US-11-297-160-8  
Sequence 8, Application US/11297160  
Publication No. US20060088888A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Xin Wei  
APPLICANT: Harris, Curtis C.  
APPLICANT: Fornace Jr., Albert J.  
APPLICANT: Courten, Jill D.  
APPLICANT: Zhan, Qimin  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by the Secretary of the  
TITLE OF INVENTION: Department of Health and Human Services  
TITLE OF INVENTION: Methods for identifying inhibitors of GADD45  
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity  
FILE REFERENCE: 015280-367100US  
CURRENT APPLICATION NUMBER: US/11/297,160  
CURRENT FILING DATE: 2005-12-07  
PRIOR APPLICATION NUMBER: US/10/600,158  
PRIOR FILING DATE: 2003-06-20  
PRIOR APPLICATION NUMBER: US/09/534,811  
PRIOR FILING DATE: 2000-03-24  
PRIOR APPLICATION NUMBER: US 60/126,069  
PRIOR FILING DATE: 1999-03-25  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 165  
TYPE: PRT  
ORGANISM: Mus musculus  
FEATURE:  
OTHER INFORMATION: mouse growth arrest and DNA-damage-inducible  
US-11-297-160-8

Query Match 54.7%; Score 451.5; DB 7; Length 165;  
Best Local Similarity 53.9%; Pred. No. 1.1e-41;  
Matches 90; Conservative 24; Mismatches 42; Indels 11; Gaps 3;

QY 1 MTLSEVRGQDTPVPESTARMOGAKALHELLLSAOROGCLTAGYSAKVLNPDVPTFC 60  
1 MTLSEFSAGE---QKTERMDKVGDALAEVLSKALSQRITVGVYEAKLINDPNDVVLJC 57  
Db 61 VLAAGEDEGDIALQIHFTLIQAFCCENDIDIVRGDVORLAIV-----GAGEBAG 113  
58 LLAADDDDDRDVALQIHFTLIQAFCCENDINILRVSNPRLAELLLETDAGPAASEGAE 117  
QY 114 -PDGLHCILISNPNEDAMKDPALFKLSLFCESRSVNDWVPSTLPE 159  
118 QPDLHCVLVTPHSSQWKDPALSLICFCRESRYMDQWVPVNIPE 164  
Db

RESULT 5  
US-11-297-160-6  
Sequence 6, Application US/11297160  
Publication No. US20060088888A1

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GENERAL INFORMATION:
APPLICANT: Wang, Xin Wei
APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Courseen, Jill D.
APPLICANT: Zhan, Qimin
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods for identifying inhibitors of GADD45
TITLE OF INVENTION: Methods for identifying inhibitors of GADD45
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REFERENCE: 015280-367100US
CURRENT APPLICATION NUMBER: US/11/297,160
PRIORITY FILING DATE: 2005-12-07
PRIORITY FILING DATE: 2003-06-20
PRIORITY FILING DATE: 2000-03-24
PRIORITY FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
2 ID NO 6
LENGTH: 160
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human growth arrest and DNA-damage-inducible
-297-160-6

Query Match
Local Similarity 54.1%; Score 447; DB 7; Length 160;
Conservative 26; Mismatches 37; Indels 10; Gaps 3;

1 MTLEEVRGODTVESTARMQAGAKALHELLLSAQRGCLTAGYSESAYLVNDPNDVTC 60
1 MTLEEFSAAE---QKTERMDTVGDALAEVLSKRSQRTITVGYEAKILNVDPDVLC 57
61 VLAAGEDEGDIALQIHFTLIQAFCCNDIDIVRGDVORLAIVGAGEBAGPG----- 115
58 LLADEEDDDRDVALQIHFTLIQAFCCNDINILRVNSPGRLELLLENDKSPAESGGLA 117
116 DLHCLVLTNPHTDAKSHGLVEVAVSYCESRSGNNQWVPYISLQ 159
116 DLHCLVLTNPHTDAKSHGLVEVAVSYCESRSGNNQWVPYISLQ 159

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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 165
TYPE: PRT
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: rat growth arrest and DNA-damage-inducible protein
OTHER INFORMATION: (rGADD45)
US-11-297-160-9

Query Match
Local Similarity 52.8%; Score 436.5; DB 7; Length 165;
Conservative 25; Mismatches 42; Indels 13; Gaps 3;

1 MTLEEVRGODTVESTARMQAGAKALHELLLSAQRGCLTAGYSESAYLVNDPNDVTC 60
1 MTLEEFSAAE---QKTERMDTVGDALAEVLSKRSQRTITVGYEAKILNVDPDVLC 57
61 VLAAGEDEGDIALQIHFTLIQAFCCNDIDIVRGDVORLAIVGAGEBAGPG-----GAGEEA 111
58 LLADEEDDDRDVALQIHFTLIQAFCCNDINILRVNSPGRLELLLENDKSPAESGGLA 117
112 GAPDLCILISNPNEDAKMDPALEKLSLFCESRSVNDVPSITLPE 159
118 QTP-DLHCVLTNPHTDAKSHGLVEVAVSYCESRSGNNQWVPYISLQ 164

RESULT 7
US-11-297-160-16
Sequence 16, Application US/11297160
Publication No. US2006008888A1
GENERAL INFORMATION:
APPLICANT: Wang, Xin Wei
APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Courseen, Jill D.
APPLICANT: Zhan, Qimin
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods for identifying inhibitors of GADD45
TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REFERENCE: 015280-367100US
CURRENT APPLICATION NUMBER: US/11/297,160
PRIORITY FILING DATE: 2005-12-07
PRIORITY FILING DATE: 2003-06-20
PRIORITY FILING DATE: 2000-03-24
PRIORITY FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 46
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:exemplary
OTHER INFORMATION: peptide inhibiting GADD45-related dissociation of
OTHER INFORMATION: Cdc2/cyclin B1 complexes
US-11-297-160-16

Query Match
Local Similarity 24.2%; Score 200; DB 7; Length 46;
Conservative 6; Mismatches 4; Indels 0; Gaps 0;

45 ESAKVLAVNDPNDVTCFLAAGEDEGDIALQIHFTLIQAFCCNDI 90
1 EAAKILAVNDPNDVTCFLAAGEDEGDIALQIHFTLIQAFCCNDI 46

RESULT 8

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-297-160-32
; Sequence 32, Application US/11297160
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xin Wei
; APPLICANT: Harris, Curtis C.
; APPLICANT: Fornace Jr., Albert J.
; APPLICANT: Courseen, Jill D.
; APPLICANT: Zhan, Qimin
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods for identifying inhibitors of GADD45
; FILE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
; LE REFERENCE: 015280-367100US
; PARENT APPLICATION NUMBER: US/11/297,160
; PARENT FILING DATE: 2005-12-07
; FOR APPLICATION NUMBER: US/10/600,158
; FOR FILING DATE: 2003-06-20
; FOR APPLICATION NUMBER: US/09/534,811
; FOR FILING DATE: 2000-03-24
; FOR APPLICATION NUMBER: US 60/126,069
; FOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; ID NO 32
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:exemplary
; OTHER INFORMATION: peptide inhibiting GADD45-related dissociation of
; OTHER INFORMATION: Cdc2/cyclin B1 complexes
-297-160-32

cy Match      22.3%; Score 184; DB 7; Length 41;
; Local Similarity 80.5%; Pred. No. 1,4e-13;
; Mismatches 4; Indels 0; Gaps 0;

50 LNVDPNVTFCVLAAGEDEGDIALQIHFTLIQAFCCENDI 90
|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 LNVDPNVTFCVLAAGEDEGDIALQIHFTLIQAFCCENDI 41

-297-160-17
; Sequence 17, Application US/11297160
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xin Wei
; APPLICANT: Harris, Curtis C.
; APPLICANT: Fornace Jr., Albert J.
; APPLICANT: Courseen, Jill D.
; APPLICANT: Zhan, Qimin
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods for identifying inhibitors of GADD45
; FILE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
; LE REFERENCE: 015280-367100US
; PARENT APPLICATION NUMBER: US/11/297,160
; PARENT FILING DATE: 2005-12-07
; FOR APPLICATION NUMBER: US/10/600,158
; FOR FILING DATE: 2003-06-20
; FOR APPLICATION NUMBER: US/09/534,811
; FOR FILING DATE: 2000-03-24
; FOR APPLICATION NUMBER: US 60/126,069
; FOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; ID NO 17
; LENGTH: 38
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:exemplary
; OTHER INFORMATION: peptide inhibiting GADD45-related dissociation of
; OTHER INFORMATION: Cdc2/cyclin B1 complexes
us-11-297-160-17

Query Match      19.9%; Score 164; DB 7; Length 38;
; Best Local Similarity 76.3%; Pred. No. 1,4e-11;
; Mismatches 29; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      49 VNVPDNTFCVLAAGEDEGDIALQIHFTLIQAFCC 86
|||||:|||||:|||||:|||||:|||||:|||||
Db      1 LNVDPNVTFCVLAAGEDEGDIALQIHFTLIQAFCC 38

RESULT 10
us-11-297-160-31
; Sequence 31, Application US/11297160
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xin Wei
; APPLICANT: Harris, Curtis C.
; APPLICANT: Courseen, Jill D.
; APPLICANT: Zhan, Qimin
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Methods for identifying inhibitors of GADD45
; FILE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
; LE REFERENCE: 015280-367100US
; CURRENT APPLICATION NUMBER: US/11/297,160
; PARENT FILING DATE: 2005-12-07
; FOR APPLICATION NUMBER: US/10/600,158
; FOR FILING DATE: 2003-06-20
; FOR APPLICATION NUMBER: US/09/534,811
; FOR FILING DATE: 2000-03-24
; FOR APPLICATION NUMBER: US 60/126,069
; FOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:exemplary
; OTHER INFORMATION: peptide inhibiting GADD45-related dissociation of
; OTHER INFORMATION: Cdc2/cyclin B1 complexes
us-11-297-160-31

Query Match      19.0%; Score 157; DB 7; Length 36;
; Best Local Similarity 77.8%; Pred. No. 7,4e-11;
; Mismatches 28; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      55 DNVTFCVLAAGEDEGDIALQIHFTLIQAFCCENDI 90
|||||:|||||:|||||:|||||:|||||:|||||
Db      1 DNVTFCVLAAGEDEGDIALQIHFTLIQAFCCENDI 36

RESULT 11
us-11-297-160-10
; Sequence 10, Application US/11297160
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xin Wei
; APPLICANT: Harris, Curtis C.
; APPLICANT: Fornace Jr., Albert J.
; APPLICANT: Courseen, Jill D.
; APPLICANT: Zhan, Qimin
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the

```

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APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
SITE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REFERENCE: 015280-367100US
CURRENT APPLICATION NUMBER: US/11/297,160
CURRENT FILING DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/10/600,158
PRIOR FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
) ID NO 10
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human GADD45 residues 58-91
-297-160-10

Try Match      17.3%; Score 143; DB 7; Length 34;
at Local Similarity 76.5%; Pred. No. 2.2e-09;
Residues 26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

61 VIAGGEDEGDIALQIHFTLLQAFCCENIDIVR 94
:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
1 LIADEDDRDVALQIHFTLLQAFCCENIDILR 34

-297-160-11

Sequence 11, Application US/11297160
Application No. US20060088888A1
GENERAL INFORMATION:
APPLICANT: Wang, Xin Wei
APPLICANT: Harris, Curtis C.
APPLICANT: Fornace Jr., Albert J.
APPLICANT: Coursen, Jill D.
APPLICANT: Zhan, Qimin
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
SITE OF INVENTION: Polypeptide Activity, and Inhibitors of Such Activity
FILE REFERENCE: 015280-367100US
CURRENT APPLICATION NUMBER: US/11/297,160
CURRENT FILING DATE: 2005-12-07
PRIOR APPLICATION NUMBER: US/10/600,158
PRIOR FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US/09/534,811
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/126,069
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
) ID NO 11
LENGTH: 34
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:human GADD45
OTHER INFORMATION: residues 58-91 with residues 62-67 changed to Ala
OTHER INFORMATION: by site-directed mutagenesis (M62-67)
-297-160-11

Try Match      15.3%; Score 126; DB 7; Length 34;
at Local Similarity 70.6%; Pred. No. 1.5e-07;
Residues 24; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

61 VIAGGEDEGDIALQIHFTLLQAFCCENIDIVR 94
:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

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Db          1 LIAAAAAAAAAADVALQIHFTLIQAFCNCENDINILR 34

RESULT 13
; Sequence 23, Application US/11297160
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xin Wei
; APPLICANT: Harris, Curtis C.
; APPLICANT: Fornace Jr., Albert J.
; APPLICANT: Coursen, Jill D.
; APPLICANT: Zhan, Qimin
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
; TITLE OF INVENTION: Poly peptide Activity, and Inhibitors of Such Activity
; FILE REFERENCE: 015280-367100US
; CURRENT APPLICATION NUMBER: US/11/297,160
; PRIOR APPLICATION NUMBER: US/10/600,158
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/534,811
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,069
; PRIOR FILING DATE: 1999-03-25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:exemplary
OTHER INFORMATION: peptide inhibiting GADD45-related dissociation of
OTHER INFORMATION: CdC2/cyclin B1 complexes
US-11-297-160-23

Query Match      14.9% Score 123; DB 7; Length 27;
Best Local Similarity 81.5%; Pred. No. 2.3e-07;
Matches 22; Conservative 3; Mismatches 2; Indels 0; Gaps 0.

QY      64 AGEDEGDIALQIHFTLIQAFCNCENDI 90
       |||::|||:|||:|||:|||
Db      1 ADEDDDRVALQIHFTLIQAFCNCENDI 27

RESULT 14
US-11-297-160-22
; Sequence 22, Application US/11297160
; Publication No. US2006008888A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Xin Wei
; APPLICANT: Harris, Curtis C.
; APPLICANT: Fornace Jr., Albert J.
; APPLICANT: Coursen, Jill D.
; APPLICANT: Zhan, Qimin
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45
; TITLE OF INVENTION: Poly peptide Activity, and Inhibitors of Such Activity
; FILE REFERENCE: 015280-367100US
; CURRENT APPLICATION NUMBER: US/11/297,160
; PRIOR APPLICATION NUMBER: US/10/600,158
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/09/534,811
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/126,069
; PRIOR FILING DATE: 1999-03-25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NOS: 32

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